From: Mertz, Prema
Sent: Tuesday, December 20, 2005 12:42 PM
To: STIC-Biotech/ChemLib
Subject: 10/789,251

Please search SEQ ID NO2 with protein databases.

Please search SEQ ID NO:26 with DNA databases.

Please search SEQ ID NO:2, 26 with US PG PUB databases.

Thanks.

Prema Mertz, Ph.D., J.D.
Primary Examiner
Art Unit 1646
4D81 Remsen Bldg Mailbox 4C70
US Patent & Trademark Office
Tel # (571) 272-0876
FAX # (571) 273-0876

****
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

****
Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

This Page Blank (unused)

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: December 24, 2005, 10:22:43 ; Search time 16 seconds
(without alignments)
1058.384 Million cell updates/sec

Title: US-10-789-251-2
Perfect score: 910
Sequence: 1 MKASSLAFSLLSAAFVLLWT..........AVVKALGELDILLQWMEETE 176

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	156.5	17.2	178	2	A38580	interleukin-10 pre
2	155	17.0	170	1	QQBE2	BCRF1 protein - hu
3	155	17.0	175	2	I46591	interleukin 10 - P
4	147.5	16.2	179	2	A48558	interleukin 10 hom
5	144	15.8	178	2	A34853	interleukin-10 pre
6	136	14.9	178	2	JN0475	interleukin-10 pre
7	94.5	10.4	567	2	JC5538	Rab geranylgeranyl
8	94.5	10.4	567	2	A45977	Rab geranylgeranyl
9	93.5	10.3	809	2	S64594	Rab geranylgeranyl
10	85	9.3	140	2	F83128	probable beta-adap
11	81.5	9.0	646	2	T33346	probable transcrip
12	81	8.9	542	2	S46367	protein kinase CDC
13	80	8.8	542	2	T19925	hypothetical prote
14	76.5	8.4	502	2	AD3160	2-isopropylmalate
15	76.5	8.4	553	2	B90153	hypothetical prote
16	76	8.4	523	2	S64826	probable membrane
17	76	8.4	917	2	T21870	hypothetical prote
18	75	8.2	276	2	B71517	hypothetical prote
19	75	8.2	726	2	T48023	ATP-dependent RNA
20	75	8.2	726	2	E83640	probable synechocy
21	75	8.2	729	2	D71302	probable pre-mRNA
22	74.5	8.2	121	2	E83640	hypothetical prote
23	74.5	8.2	1047	2	H69879	probable exonuclea
24	74	8.1	682	2	B71917	ATP-dependent DNA
25	73.5	8.1	449	2	D87602	udp-n-acetylmurama
26	73.5	8.1	653	2	F97321	sensory box histid
27	73.5	8.1	729	2	S33945	membrane export pr
28	73.5	8.1	782	2	A98211	late protein, 100K
29	73.5	8.1	794	2	C86057	hypothetical prote
30	73	8.0	471	2	B38637	Ras inhibitor (clo
31	73	8.0	563	2	D90531	excinuclease ABC s
32	73	8.0	614	2	E83880	hypothetical prote
33	73	8.0	1008	2	D84434	probable receptor-
34	72.5	8.0	261	2	H98213	transcription repr
35	72.5	8.0	388	2	T00641	hypothetical prote
36	72.5	8.0	409	2	A54750	TNF receptor assoc
37	72.5	8.0	447	2	T20552	ywbL protein - Bac
38	72.5	8.0	481	2	S39682	hypothetical prote
39	72.5	8.0	481	2	T33153	hypothetical prote
40	72.5	8.0	1101	2	AF2545	variant-specific s
41	72.5	8.0	2182	2	F81833	hypothetical prote
42	72.5	7.9	2581	2	E81197	conserved hypothet
43	72	7.9	255	2	A70081	conserved hypothet
44	72	7.9	279	2	S74651	hypothetical prote
45	72	7.9	351			

ALIGNMENTS

RESULT 1
A38580
interleukin-10 precursor - human
N;Alternate names: cytokine synthesis inhibitory factor (CSIF); IL-10
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1992 #sequence revision 14-Feb-1992 #text_change 09-Jul-2004
A;Accession: A38580; G01539; G37890
R;Vieira, P.; de Waal-Malefyt, R.; Dang, M.N.; Johnson, K.E.; Kastelein, R.; Florentin
Proc. Natl. Acad. Sci. U.S.A. 88, 1172-1176, 1991
A;Cross-references: UNIPROT:P22301; UNIPARC:UPI000000034E50; GB:M57627; NID:g186270; PID
A;Title: Isolation and expression of human cytokine synthesis inhibitory factor cDNA c
R;Windsor, W.T.; Syto, R.; Tsarbopoulos, A.; Zhang, R.; Durkin, J.; Baldwin, S.; Paliw
Biochemistry 32, 8807-8815, 1993
A;Cross-references: A38580; MUID:91142134; PMID:1847510
A;Title: Disulfide bond assignments and secondary structure analysis of human and muri
A;Reference number: A48693; MUID:93372085; PMID:8364028
A;Contents: annotation; disulfide bonds in recombinant protein
R;Sanjanwala, B.
submitted to the EMBL Data Library, October 1994
A;Reference number: G07695
A;Accession: G01539
A;Molecule type: DNA
A;Residues: 1-178 <SAN>
A;Cross-references: UNIPARC:UPI000000178477; EMBL:X78437; NID:g1167482
R;Platzer, C.; Volk, H.D.; Platzer, M.
DNA Seq. 4, 399-401, 1994
A;Title: 5' noncoding sequence of human IL-10 gene obtained by oligo-cassette PCR walk
A;Reference number: I37890; MUID:95143580; PMID:7841462
A;Accession: I37890
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-6 <PLA>
A;Cross-references: UNIPARC:UPI000011E9B9; EMBL:X73536; NID:g452395; PIDN:CAA51942.1;
C;Genetics:
A;Gene: GDB:IL10; IL-10
A;Cross-references: GDB:128636; OMIM:124092
A;Map position: 1q31-1q32
A;Introns: 55/3; 75/3; 126/3; 148/3
C;Superfamily: interleukin-10

RESULT 1
A38580
interleukin-10 precursor - human
N;Alternate names: cytokine synthesis inhibitory factor (CSIF); IL-10
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1992 #sequence revision 14-Feb-1992 #text_change 09-Jul-2004
A;Accession: A38580; G01539; G37890
R;Vieira, P.; de Waal-Malefyt, R.; Dang, M.N.; Johnson, K.E.; Kastelein, R.; Florentin
Proc. Natl. Acad. Sci. U.S.A. 88, 1172-1176, 1991
A;Cross-references: UNIPROT:P22301; UNIPARC:UPI000000034E50; GB:M57627; NID:g186270; PID
A;Title: Isolation and expression of human cytokine synthesis inhibitory factor cDNA c
R;Kube, D.; Platzer, C.; von Knethen, A.; Straub, H.; Hafner, M.; Tesch, H.
submitted to the EMBL Data Library, March 1994
A;Reference number: S49110
A;Description: Isolation of the human interleukin-10-promoter. Characterization of the
A;Reference number: S49110
A;Accession: S49110
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-6, 'PVAWSS' <KUB>
A;Cross-references: UNIPARC:UPI000001E9B9;

```
C;Keywords: cytokine; glycoprotein; lymphokine; T-cell
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-178/Product: interleukin-10 #status predicted <MAT>
F;30-126,80-132/Disulfide bonds: #status experimental
F;134/Binding site: carbohydrate (Asn) (covalent) #status predicted
```

```
Query Match          156.5; DB 2; Length 178;
Best Local Similarity 27.4%; Pred. No. 8.1e-08;
Matches   43; Conservative 32; Mismatches 71; Indels 11; Gaps 5;

Qy   22 STGLKTNLGSCV----IATNLQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQDTKP 76
              :::||:|| | :|  |||:|:::||||||||||||||||||||||||||||
Db   19 SPGQGTQSENSCTHFPGNLPNMLRDLRDAFSRVKTFFQMKD-QLD-NLLKESLLEDFRKG 76

Qy   77 ANRCCLLRHLLRLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGE 136
              ||||||||||||||||  :| |||||||| |||||||||||||||||||||||||||
Db   77 YLGCQALSEMIQFYLEEVMPQAENQDPDIKAHVNSLGENLKTLRLRRCHRFLPC--E 133

Qy  137 EAAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWME 173
              |:|||||||||||||||||||:|:|||||||||||||
Db  134 NKSKAVEQVKNAFNKLQ-EKGIYKAMSEFDIFINYIE 169
```

```
RESULT 2
QQBE2
BCRF1 protein - human herpesvirus 4 (strain B95-8)
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A;Reference number:  A03741; S32974
A;Accession: A03741
A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
A;Reference number: A93065; MUID:85035713; PMID:6092825
A;Accession: A03741
A;Molecule type: DNA
A;Residues: 1-170 <BAN>
A;Cross-references: UNIPROT:P03180; UNIPARC:UPI0000000CDBE; EMBL:V01555; NID:g559074; PIDN
R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
Nature 310, 207-211, 1984
A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A;Reference number: A03794; MUID:84270667; PMID:6087149
A;Contents: annotation; protein coding region
C;Superfamily: interleukin-10
```

```
Query Match          17.2%; Score 155; DB 1; Length 170;
Best Local Similarity 28.9%; Pred. No. 1.1e-07;
Matches   39; Conservative 29; Mismatches 61; Indels 6; Gaps 4;

Qy   39 LQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLRLYLDRVFKNY 98
              ::| :||||||||||||||||||||||||||||||:||||  :||||||||| :|
Db   34 LRDLRDAFSRVKTFFQTKD-EVD-NLLKESLLEDFKGYLGCQALSEMIQFYLEEVMPQA 91

Qy   99 QTPDHYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAV 158
              ||||||||| :|||| ||||| |||:||:||||||||| |||||||||||||||||||
Db   92 ENQDPEAKDHVNSLGENLKTLRLRRCHRFLPC--ENKSKAVEQIKNAFNKLQ-EKGI 147

Qy  159 VKALGELDILLQWME 173
              |:|||||||||||:|
Db  148 YKAMSEFDIFINYIE 162
```

```
RESULT 3
I46591
interleukin 10 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46591
R;Blancho, G.; Gianello, P.; Germana, S.; Baetscher, M.; Sachs, D.H.; LeGuern, C.
Proc. Natl. Acad. Sci. U.S.A. 92, 2800-2804, 1995
A;Title: Molecular identification of porcine interleukin 10: regulation of expression in
A;Reference number: I46591; MUID:95224028; PMID:7708727
A;Accession: I46591
A;Status: preliminary; translated from GB/EMBL/DDBJ
```

```
A;Molecule type: mRNA
A;Residues: 1-175 <BLA>
A;Cross-references: UNIPROT:Q29055; UNIPARC:UPI000012D476; GB:L20001; NID:g309792; PIDN
C;Genetics:
A;Gene: IL-10
C;Superfamily: interleukin-10

Query Match          17.0%; Score 155; DB 2; Length 175;
Best Local Similarity 27.0%; Pred. No. 1.1e-07;
Matches   48; Conservative 34; Mismatches 78; Indels 18; Gaps 6;

Qy   22 STGLKTNLGSCV-----IATNLQEIRNGFSDIRGSVQA 55
              |||| | |::|:    :|||::||||||||||||||||
Db    1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCV-----IATNLQEIRNGFSDIRGSVQA 55

Qy   56 KDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLRLYLDRVFKNYQTPDHYTLRKISSLANS 115
              |||||||||||||||||||||||||||||||||||||||||||||:| |||||||||||
Db    1 MPSSALLYCLI-----PLAGVAASIKSEN--SCIHFPTSLPHMLRELRAAFGPVKSFFPQT 53

Qy  116 FLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWME 173
              |:||:| |||:||:||||||| |||||||||||||||||||||||:||||||||||
Db   54 KDQMGD--LLLTGSLLEDFRKGYLGCQALSEMIQFYLEDVMPKAESDGEDIKEHVNSLGEK 111

Qy                                                              173
Db  112 LKTLRLRLRRCHQFLPC---ENKSKAVEEVKSAFSKLQ-ERGVYKAMGEFDIFINYIE 165
```

```
RESULT 4
A48558
interleukin 10 homolog - equine herpesvirus 2
N;Alternate names: hypothetical protein E7
C;Species: equine herpesvirus 2
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: A48558; S55664
R;Rode, H.J.; Janssen, W.; Rosen-Wolff, A.; Bugert, J.J.; Thein, P.; Becker, Y.; Darai,
Virus Genes 7, 111-116, 1993
A;Title: The genome of equine herpesvirus type 2 harbors an interleukin 10 (IL10)-like
A;Reference number: A48558; MUID:93227565; PMID:8385838
A;Accession: A48558
A;Molecule type: DNA
A;Residues: 1-179 <ROD>
A;Cross-references: UNIPROT:Q89451; UNIPARC:UPI000012D058; GB:U20824; NID:g695172; PIDN:AAC13857.1; PID
A;Note: sequence extracted from NCBI backbone (NCBIN:129334, NCBIP:129335)
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
C;Superfamily: interleukin-10
```

```
Query Match          17.0%; Score 147.5; DB 2; Length 179;
Best Local Similarity 31.9%; Pred. No. 6.1e-07;
Matches   44; Conservative 24; Mismatches 59; Indels 11; Gaps 6;

Qy   39 LQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLRLYLDRVFKNY 98
              ::| :||||||||||||||||||||||||||||||:||||  :|||||||||||:|
Db   41 LHELRAAFSRVKTFFQMKD-QLD-NMLLDGSLLEDFKGYLGCQALSEMIQFYLEEVMP-- 96

Qy   99 QTPDHYTLR--KISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQ 155
              |||||||||  :|||| |||:| |||:||:||||||| ||||||||||||||||||||
Db   97 QAENHSTDQEKDKVNSLGEKLKTLRLRRCHRFLPC---ENKSKAVEQVKSAFSKLQ-E 152

Qy  156 AAVVKALGELDILLQWME 173
              ||:|:|||||||||||:|
Db  153 KGVYKAMSEFDIFINYIE 170
```

```
RESULT 5
A34853
interleukin-10 precursor - mouse
```

N;Alternate names: cytokine synthesis inhibitory factor (CSIF); IL-10
C;Species: Mus musculus (house mouse)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
A;Residues: 1-178 <MOO>
R;Kim, J.M.; Brennan, C.I.; Copeland, N.G.; Jenkins, N.A.; Khan, T.A.; Moore, K.W.
J;Immunol. 148, 3618-3623, 1992
A;Title: Structure of the mouse IL-10 gene and chromosomal localization of the mouse and
A;Reference number: I56136; MUID:92268508; PMID:1350294
A;Accession: I56136
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-178 <RES>
A;Cross-references: UNIPARC:UPI000002149E; GB:M84340; NID:g198291; PIDN:AAA39275.1; PID:
C;Genetics:
A;Gene: IL10
C;Superfamily: interleukin-10
C;Keywords: cytokine; lymphokine; T-cell

```
Query Match     15.8%;  Score 144;  DB 2;  Length 178;
Best Local Similarity   31.1%;
Matches   42;  Conservative   19;  Mismatches   68;  Indels    6;  Gaps    4;

Qy   39 LQEIRNGFSDIRGSVQAKDGNIDIRIRLRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNY  98
            ||  |    |:|:|  |  |  ::   || ||: ::
Db   41 LLELRTAFSQVKTFPQTKD-QLD-NILLTDSLMQDFKGYLGCQALSEMIQFYLVEVMPQA  98

Qy   99 QTPDHYTLRKISSLANSFLTIKKDLRLCHAHMTCHGGEEAMKKYSQILSHFEKLEPQAAV 158
            :|||
Db   99 EKHGPEIKEHLNSLGEKLKTLRMRLRRCHRFLPC---ENKSKAVEQVKSDFNKLQDQ-GV 154

Qy  159 VKALGELDILLQWME 173
            |:|  ::|   |
Db  155 YKAMNEFDIFINCIE 169
```

RESULT 6
JN0475
interleukin-10 precursor - rat
N;Alternate names: cytokine synthesis inhibitory factor
N;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JN0475; JC1357; S36021
R;Feng, L.; Tang, W.W.; Chang, J.C.C.; Wilson, C.B.
Biochem. Biophys. Res. Commun. 192, 452-458, 1992
A;Title: Molecular cloning of rat cytokine synthesis inhibitory factor (IL-10) cDNA and
A;Reference number: JN0475
A;Accession: JN0475
A;Molecule type: mRNA
A;Residues: 1-178 <FEN>
A;Cross-references: UNIPROT:P29456; UNIPARC:UPI000016795 9
R;Goodman, R.E.; Oblak, J.; Bell, R.G.
Biochem. Biophys. Res. Commun. 189, 1-7, 1992
A;Title: Synthesis and characterization of rat interleukin-10 (IL-10) cDNA clones from t
A;Reference number: JC1357; MUID:93080542; PMID:1280414
A;Accession: JC1357
A;Molecule type: mRNA
A;Residues: 1,'P',3-64,'L',66-178 <GOO>
A;Cross-references: UNIPARC:UPI000012D477; GB:L02926; NID:g204903; PIDN:AAA41425.1; PID:
R;Feng, L.
submitted to the EMBL Data Library, July 1991
A;Reference number: S36021
A;Accession: S36021

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-178 <FE2>
A;Cross-references: UNIPARC:UPI000001679S5; EMBL:X60675; NID:g296620; PIDN:CAA43090.1;
C;Superfamily: interleukin-10
C;Keywords: cytokine; glycoprotein; lymphokine; T-cell
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-178/Product: interleukin-10 #status predicted <MAT>
F;19-178/Domain: interleukin-10 #status predicted
F;29,134/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Query Match     14.9%;  Score 136;  DB 2;  Length 178;
Best Local Similarity   28.5%;
Matches   53;  Conservative   26;  Mismatches   77;  Indels   30;  Gaps    8;

Qy    1 MKASSLAPSLLSAAFYLLWTPSTGLKTLNLGSCVIATN-------------LQEIRNGFSD  48
        | :| ||  :|| |      ||||  |:   |  :                 :|  ||
Db    1 MLGSALLCLLLLA------------GVKT-SKGHSIRGDNNCTHFPVSQTHMLRELRAAFSQ 50

Qy   49 IRGSVQAKDGNIDIRIRLRRTES-LQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLR 107
        ::   :|  ||:| || | ::  |||  | |  ||| :::| ||||| |
Db   51 VKTFPQKKD-QLDNIVL--TDSLLQDFKGYLGCQALSEMIKFYLVEVMPQAENHGPEIKE 107

Qy  108 KISSLANSFLTIKKDLRLCHAHMTCHGGEEAMKKYSQILSHFEKLEPQAAVVKALGELDI 167
           |:| |  | :|| : | | : | ||| | ||||||   |  :||  | :|  ||:|
Db  108 HLNSLGEKLKTLWIQLRRCHRFLPC---ENKSKAVEQVKNDFNKLQDK-GVYKAMNEFDI 163

Qy  168 LLQWME 173
             :|
Db  164 FINCIE 169
```

RESULT 7
JC5538
Rab geranylgeranyl transferase (EC 2.5.1.-) alpha chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
A;Accession: JC5538
R;Song, H.J.; Rossi, A.; Ceci, R.; Kim, I.G.; Anzano, M.A.; Jang, S.I.; De Laurenzi, V
Biochem. Biophys. Res. Commun. 235, 10-14, 1997
A;Title: The genes encoding geranylgeranyl transferase alpha-subunit and transglutamin
A;Reference number: JC5538; MUID:97339427; PMID:9196026
A;Accession: JC5538
A;Molecule type: DNA
A;Residues: 1-567 <SON>
A;Cross-references: UNIPROT:Q92696; UNIPARC:UPI0000131BBB
C;Comment: This protein is involved in cutaneous disease. The gene of this enzyme is p
C;Genetics:
A;Gene: Rabggta
A;Introns: 1/3; 38/3; 81/1; 143/1; 238/2; 278/3; 300/3; 336/2; 354/2; 383/2; 41
C;Keywords: transferase

```
Query Match     10.4%;  Score 94.5;  DB 2;  Length 567;
Best Local Similarity   25.8%;
Matches   49;  Conservative   26;  Mismatches   82;  Indels   33;  Gaps    9;

Qy    1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQE--IRNGFSD---IRGSVQA 55
        | :|| |:: ||:|    |   : ||:|  | :           :|||:|      |:
Db    1 LPAASLNDQLPQHTFRVIWIRAGDVQK-----ECVLLKGROEGWCRDSTTDEQLFRCELSV 358

Qy   56 KDGNIDIRIRLRRTESLQDTKPANRCCLLRHLL------------RLYLDRVFKNYQT---- 103
        | |  | |: : :||  |  : |    |  ||             ||||   ||
Db  304 LPAASLNDQLPQHTFRVIWIRAGDVQK-----ECVLLKGROEGWCRDSTTDEQLFRCELSV 358

Qy  104 YT-----LRKISSLANSFLTIK----KDLRLCHAHMTCHGGEEAMKKYSQI-LSH--FEKL 152
        |       ||:|| |  | :||    ||  | | | : | |:   |   :| |:    |:|
Db  359 EKSTVLQSBLESCKELQELBPENKWCLLTILLMRALDPLIYEKETLQYFQTLKAVDPMR 418

Qy  153 EPQAAVVKAL 162
        :|  || :|
Db  419 ATYLDLDRSKFLLENSVLKMEYAEVRVIHLAHKDLTVLCHLEQLLLVTHLDLSHRLRTL 478

Qy  153 EPQAAVVKAL 162
          :| :|||
Db  479 PPALAALRCL 488
```

RESULT 8

A45977
A;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A45977
R;Armstrong, S.A.; Seabra, M.C.; Sudhof, T.C.; Goldstein, J.L.; Brown, M.S.
J. Biol. Chem. 268, 12221-12229, 1993
A;Title: cDNA cloning and expression of the alpha and beta subunits of rat Rab geranylge
A;Reference number: A45977; MUID:93280201; PMID:8505342
A;Accession: A45977
A;Molecule type: mRNA; protein
A;Residues: 1-567 <ARM>
A;Cross-references: UNIPROT:Q08602; UNIPARC:UPI0000133188F; GB:S62096; NID:g385474; PIDN:
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIN:133369, NCBIP:133370)

Rab geranylgeranyl transferase component B alpha subunit - rat

Best Local Similarity   10.4%;
Matches   46; Conservative   31; Mismatches   80; Indels   33; Gaps   8;

Qy   1 MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQE--IRNGFSD---IRGSVQA 55
            :   : : :: :|| : | : ::   : : :| | : ::
Db   304 LPAASLNDQLPQHFFRVIWTGSDSQK------ECVLLKDRPECWCRDSAYDEQLFRCELSV 358

Qy   56 KDGNIDIRILRRTESLQDTFKPANRCCLLRHLLRL--YLDRVFKNYQTPDHYT------- 105
            :|| || ||::   : | : :: : : || :|| |
Db   359 EKSTVLQSELESCKELQELRPENKWCLLIIILLMRALDPLLYEKETLQYFSTLKAVDPMR 418

Qy   106 ------LRKISSLANSFLITK----KDLRLCHAHMTCHCGGEAMKKYSQI-LSH--FEKL 152
                  ||| : :: :|| :|| | |||| | || | :   :||
Db   419 AAYLDDLRSKFLLENSVLKMEYADVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRAL 478

Qy   153 EPQAAVVKAL 162
              :   : |:
Db   479 PPALAALRCL 488

RESULT 9
S64594
probable beta-adaptin YKS5 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein G9331; protein YGR261c
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: S64594; S63450
R;Panzeri, L.; Agostoni Carbone, M.L.; Melchioretto, P.; Plevani, P.; Martegani, E.; Var
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64591
A;Accession: S64594
A;Molecule type: DNA
A;Residues: 1-809 <PAN>
A;Cross-references: UNIPROT:P46682; UNIPARC:UPI00000530A8; EMBL:Z73046; NID:g1323474; PI
A;Experimental source: strain S288C
R;Robinson, L.C.; Engle, H.M.; Panek, H.R.
submitted to the EMBL Data Library, September 1995
A;Description: Suppressors of loss of yeast casein kinase 1 function define the four sub
A;Reference number: S63439
A;Accession: S63450
A;Molecule type: DNA
A;Residues: 1-26, 'PLSWNPP',36-723,'T',725-795,801-809 <ROB>
A;Cross-references: UNIPARC:UPI000016BAA1; EMBL:U35411; NID:g1017728; PID:g1017729
A;Genetics:
C;Gene: SGD:YKS5
A;Cross-references: SGD:S0003493; MIPS:YGR261c
A;Map position: 7R

Query Match   24.1%; Score 93.5; DB 2; Length 809;
Best Local Similarity   10.3%;
Matches   48; Conservative   39; Mismatches   73; Indels   39; Gaps   10;

Qy   2 KASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQARDGNID 61
            :::: || :|||| |||| :| ::||: :| :   : | |: :: :| |: ||
Db   21 EAAAVATSKLGESSTYYY--SQNINPQQLVTLLNGSRNSREVRDAMKRIISIMASDDDSID 78

RESULT 10
F83128
probable transcription regulator PA4135 [imported] - Pseudomonas aeruginosa (strain PAO1
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: F83128
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
. ; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83128
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-140 <STO>
A;Cross-references: UNIPROT:Q9HWP6; UNIPARC:UPI00000C5C2C; GB:AE004830; GB:AE004091; NIF
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA4135

Query Match   24.5%; Score 85; DB 2; Length 140;
Best Local Similarity   9.3%;
Matches   25; Conservative   25; Mismatches   42; Indels   10; Gaps   3;

Qy   62 IRI----LRRTESLQDTFKPANRCCLLRHLLRLRYLDRVFKNYQTPDHYTLRKISSLANSFL 117
           :|| |: || : | :| ::   :| | :: | : :| :| |::| |
Db   79 VQLYFADVVKNITTNDTK-------VKRLIHYLURFAEN---DPNLTLLSINSLQKSLS 128

Qy   118 TIKQDLRLCHAHMTCHCGGEAMKKYSQILSHFEK---LEPQA----AVVK-ALGE 164
           :|||||||||||| |||| ||:|||||||:||| | || :
Db   129 DSNSELR-CFA--LSALSDMKMSSLAPIILHTVKKLVTDPSAMVRGEVALAIIKLYRAGK 185

Qy   165 ------LDILLQWMEETE 176
                  | :: :: |:
Db   186 NDYHEELLDILKELMADTD 204

RESULT 11
T33346
hypothetical protein C16A11.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33346
R;Johnson, D.; Blewald, T.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of C. elegans cosmid C16A11.
A;Reference number: Z21328
A;Accession: T33346
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-646 <JOH>
A;Cross-references: UNIPROT:O76579; UNIPARC:UPI000007652553; EMBL:AF075536; PIDN:AAC26261
A;Experimental source: strain Bristol N2; clone C16A11
C;Genetics:
A;Gene: CESP:C16A11.5
A;Genetic:
A;Map position: 2
A;Introns: 35/3; 72/1; 94/3; 129/3; 184/3; 205/1; 279/3; 387/3; 505/2; 540/2; 570/3

Query Match   9.0%; Score 81.5; DB 2; Length 646;
Best Local Similarity   26.1%;
Matches   36; Conservative   22; Mismatches   49; Indels   31; Gaps   8;

Qy   62 IRILRRTESLQDTFKPANRCCLLRH-----LLRLYLDRVFKNYQTPDHYTLRKISSLANS- 115
           :||| :|| :| | ::: :: |:|:| || :: | ||
Db   40 IRILRQQGEMESYQLANQACILRPSMTGVLARLERDGIVARRWKAPKDQR-RVYVNLTEKG 98

Qy   116 ---FLITKKQDLRLCHAHMTCHCGGEAMKKYSQILSHFEKLEP 154
              |: || :|||||||||| |||| ||:||||||| ||:|||
Db   99 QQCFVSMSGDMEKNYQRIQERFGEEKLAQLLELLNELKKIKP 140

Qy 29 NLGSCVIATNLQEIRNGFSDIRGSVQAKDGNIDIRILR----------RTESLQDTKPANRC 80
         ::|:|::|:| |:|| | ||:|:
Db 176 NQGACFVDRSLEQ-RNSNGDHLPIVQELDSMKSIEFIQHPIQRAKHKAVPIEDLKPGSYC 234

Qy 81 CL-LRHLLRLYLD------RVFKNYQTPD--HYTLRKISSLANSFLTIKKDLRLCHAHMTC 132
        || |||:|||:| ||| | || ||:||||| || |||:|| |||:|
Db 235 ILAVDALFELFNEIIWGSRVFEKHKVPKIIEYVL-KIPT----LLFKSELRPHFIKTA 288

Qy 133 HCGBEAMKKYSQILSHFE 150
           ||:|| | ||| |
Db 289 H-------LHRLLASFE 298

RESULT 12
S46367
protein kinase CDC7 (EC 2.7.1.-) - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 05-Oct-2004
C;Accession: S46367; T39888
R;Pankhauser, C.; Simanis, V.
EMBO J. 13, 3011-3019, 1994
A;Title: The cdc7 protein kinase is a dosage dependent regulator of septum formation in
A;Reference number: S46367; MUID:94313982; PMID:8039497
A;Accession: S46367
A;Molecule type: DNA
A;Status: nucleic acid sequence not shown
A;Residues: 1-1062 <PAN>
A;Cross-references: UNIPROT:P41892; UNIPARC:UPI000001272259; EMBL:AL035537; PIDN:CAB36886.1; GSPDB:GN00067
A;Experimental source: strain 972h-; cosmid c21
C;Genetics:
A;Gene: CDC7; SPDB:SPBC21.06c
A;Map position: II; 2
A;Introns: 9/3; 54/3; 86/2; 171/1; 325/1; 405/3; 427/1; 544/3; 589/3
A;Description: essential for septum formation and cell division
C;Function:
A;Keywords: ATP; cell division; phosphotransferase; protein kinase
F;7-259/Domain: protein kinase homology <KIN>
F;15-23/Region: protein kinase ATP-binding motif

Query Match   8.9%;   Score 81;   DB 2;   Length 1062;
Best Local Similarity   30.2%;   Pred. No. 15;
Matches 32;   Conservative 20;   Mismatches 44;   Indels 10;   Gaps   4;

Qy 23 TGLKTLNLGSCVIATNLQEIRNG-FSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCC 81
Db 466 TGLGTLVLNKCYGSWNNENEDGEBESDIFDSIETNLENLDIE----NNIALDKRTHLAS 520

Qy 82 LLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIKKDLRLCH 127
Db 521 LLSSLLGSLRD---KNIGSKD--TTVSQIASILSEDLSLKREIIQAH 562

RESULT 13
T19925
hypothetical protein C44C10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19925
R;Cottage, A.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z19197
A;Accession: T19925
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-542 <WIL>
A;Cross-references: UNIPROT:Q18616; UNIPARC:UPI00017B837; EMBL:Z69787; PIDN:CAA93638.
A;Experimental source: clone C44C10
C;Genetics:
A;Gene: CESP:C44C10.4
A;Map position: X
A;Introns: 66/3; 229/3; 309/1; 328/3; 398/3

Query Match   8.8%;   Score 80;   DB 2;   Length 542;
Best Local Similarity   23.2%;   Pred. No. 8.5;
Matches 29;   Conservative 25;   Mismatches 43;   Indels 28;   Gaps   4;

Qy 146 LSHFE 150
          :||
Db 317 IDYTE 321

RESULT 14
AD3160
hypothetical protein glnP/glnQ [imported] - Agrobacterium tumefaciens (strain C58, Dup
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AD3160
A;Molecule type: DNA
A;Status: preliminary
A;Residues: 1-502 <KUR>
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCle
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD3160
A;Molecule type: DNA
A;Status: preliminary
A;Residues: 1-502 <KUR>
A;Cross-references: UNIPROT:Q9WWF4; UNIPARC:UPI00000D146D; GB:AE008687; PIDN:AAL45698
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: glnP/glnQ
A;Genome: plasmid

Qy 39 LQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNY 98
        |||:|||:||||||||||||||||||||||||||||
Db 212 IQETKBKFVABQLKVNAKANAKMPLRISRYSEAIPKQTPSPN---------------PKNN 256

Qy 99 -----QTPDHY----TLRKISSLANSFLTIKKDL--RLCHAHMTCHCGBEAMKKYSQI 145
            ||| | ||:||||| || |||
Db 257 AIVVRPKTHNHYDNLITVDKLNSYLNEKVTERRELLQFAVAHPNMNIRFSEEGPNIYARE 316

Qy 146 LSHFE 150
          :||
Db 317 IDYTE 321

Query Match   8.4%;   Score 76.5;   DB 2;   Length 502;
Best Local Similarity   24.6%;   Pred. No. 17;
Matches 42;   Conservative 23;   Mismatches 37;   Indels 69;   Gaps 10;

Qy 10 LISAAFYLLWT-PSTGL-----KTLNLGS---CVIATNLQEIRNGFSDIRGSVQA----- 55
Db 206 LLAGVPYLIVTVPLTHVVNAIDNRLRIGKQRPSVITSGLEBV---SELDGAARASGVAF 261

Qy 56 KDGNIDIRILRRTESLQD------------TKPANRCC-------LLRHL------ 86
Db 262 KGGSLDVRLGMAYGDLDVLKGVDLSVKPGSVTCIIGPSGSGKSTLLRGLNRLVEPKSGD 321

Qy 87 ------------LRLYLDRVFKNYQT-PDHYTLRKISSLANSFLTIKK 121
Db 322 ILIDGESILAMKPETLRRVGMVFQHFNLFPDH-----TALENVMLSLKK 366

RESULT 15
B90153
2-isopropylmalate synthase, probable (leuA-1) [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: B90153

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: B90153
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-553 <KUR>
A;Cross-references: UNIPROT:Q98OZ1; UNIPARC:UPI00000641BD; GB;AB006641; NID:g13812259; F
C;Genetics:
C;Gene: leuA-1
C;Superfamily: 2-isopropylmalate synthase leuA

Query Match   8.4%;   Score 76.5;   DB 2;   Length 553;
Best Local Similarity   19.6%;   Pred. No.19;
Matches   39;   Conservative   34;   Mismatches   61;   Indels   65;   Gaps   8;

Qy   24   GLKTLNLGSCVIATNLQBIRNGFSDIRGSVQA---KDGNID------------IRILRR   67
             |: |:|: || |: ||:::: |:
Db   232   GIHAHNDIGCAVANSLMAIKAGARHVQGTINGIGERTGNADLIQIIPTLILKMGINALNG 291

Qy   68   TESLQDTKPANRCC----------------LLRHLLRLYLDRVFKNYQTPDH------- 103
             ||||| |::| | ::|
Db   292   QESLRKLREVSRIVYEILGLPPNPYQPYVGDNNAFAHKAGVHVDAVMKVPRAYEHVDPSLV 351

Qy   104   ------YTLRKISSLAN--SFL------TIKKDLRLCHAHMTCHGGEEAMKKYSQILSHFE 150
                   : : : |:| :|::
Db   352   GNDRKFVISELSGTANLVSYLQGLGIAVDKKDERL--------KKALNKIKELEARGY   401

Qy   151   KLE--PQAAVVKALGBLDI 167
             : |:|: |||:|:|
Db   402   SFDVGPASAILITLKELNI 420

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

(This Page Blank (laspio))

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 24, 2005, 10:26:03 ; Search time 228 Seconds
(without alignments)
544.618 Million cell updates/sec

Title: US-10-789-251-2
Perfect Score: 910
Sequence: 1 MKASSLAPSLLSSAAFVLLWT............AVVKALGELDILLQWMEETE 176

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	906	99.6	176	1	IL20_HUMAN	Q9NYY1 homo sapien
2	672	73.8	176	1	IL20_MOUSE	Q9JKV9 mus musculu
3	337.5	37.1	177	1	IL19_HUMAN	Q9UHD0 homo sapien
4	337.5	37.1	215	2	Q5VUT3_HUMAN	Q5vut3 homo sapien
5	306	33.6	168	2	Q4LDR4_BRARE	Q4ldr4 brachydanio
6	281.5	30.9	176	2	IL19_MOUSE	08ci70 mus musculu
7	266.5	29.3	175	2	Q7SX60_TETNG	07sx60 tetraodon n
8	222	24.4	220	2	Q92553_MOUSE	092553 mus musculu
9	220	24.2	181	2	Q92584_MOUSE	092584 mus musculu
10	217	23.8	206	2	O13007_HUMAN	013007 homo sapien
11	217	23.8	207	2	Q53X27_HUMAN	053x27 homo sapien
12	191	21.0	183	1	IL24_HUMAN	Q13007 homo sapien
13	187	20.5	183	1	MOB5_RAT	mob5 rattus norv
14	175.5	19.3	175	2	Q9WVP8_RAT	q9wvp8 rattus norv
15	175.5	19.3	175	2	Q9J124_HUMAN	q9j124 homo sapien
16	161.5	17.7	178	1	Q6A2H5_CHICK	q6a2h5 gallus gall
17	161	17.7	177	2	Q6A2H4_CHICK	q6a2h4 gallus gall
18	157.5	17.3	178	1	IL10_MACNE	p51497 macaca neme
19	157.5	17.3	177	2	Q8UZ6_9GAMA	08uz6 cercopithec
20	157.5	17.3	178	1	IL10_MACFA	p51496 macaca fasc
21	157.5	17.3	178	1	IL10_MACMU	p79938 macaca mula
22	156.5	17.2	180	2	IL10_PAPHA	p51496 papio hamad
23	156.5	17.2	178	1	Q7T3I1_CYPCA	q7t3i1 cyprinus ca
24	156.5	17.2	160	2	Q71UZ1_HUMAN	q71uz1 homo sapien
25	156.5	17.2	178	1	Q5GOV6	q5gov6 homo sapien
26	155	17.0	170	1	IL10_FELCA	p55029 felis silve
27	155	17.0	170	2	P22301	p22301 homo sapien
28	155	17.0	175	1	Q6FGW4_HUMAN	q6fgw4 homo sapien
29	154.5	17.0	178	1	Q77H2_9GAMA	q77h2 epstein-bar
30	153	16.8	178	1	Q29055	q29055 sus scrofa
31	151.5	16.6	179	1	IL10_PIG	p26895 human herpe
32	151	16.6	178	1	Q9TSJ4	oryctolagus
33	147.5	16.2	178	2	Q9TVD3	oryctolagus
34	147.5	16.2	179	1	Q9TVD3_RABIT	sigmodon hi
35	147.5	16.2	179	1	P68678	equine herp
36	147	16.0	178	1	IL10H_EHV2	equine herp
37	145.5	16.0	178	2	P18893	mus musculu
38	144.5	15.9	160	2	Q6FGS9_HUMAN	homo sapien
39	144.5	15.9	174	1	Q6FGG9	homo sapien
40	144.5	15.9	178	1	Q923T1_SIGHI	sigmodon hi
41	143.5	15.8	178	1	O97798	trichosurus
42	143	15.7	171	2	IL10_TRIVU	trichosurus
43	142.5	15.7	178	1	IL10_HORSE	equus cabal
44	142.5	15.7	178	2	Q28374	equus cabal
45	142	15.6	181	1	Q90SL1_CHV12	cercopithec

Additional accessions appearing in the ID/AC columns for the lower‑scoring hits:
Q6VV71_BUBBU / Q90511 (bubalus bub); IL10_BOVIN / P43480 (bos taurus);
Q8MKG9_SAISC / Q8mkg9 (saimiri sci); IL10_CANFA / P48411 (canis famil);
IL10_CERTO (cercocebus); IL10_MERUN (meriones un); IL10_CEREL (cervus elap).

ALIGNMENTS

RESULT 1
IL20_HUMAN

```
ID   IL20_HUMAN     STANDARD;     PRT;   176 AA.
AC   Q9NYY1; Q96QZ6;
DT   28-FEB-2003 (Rel. 41, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Interleukin-20 precursor (IL-20) (Four alpha helix cytokine Zcyto10).
GN   Name=IL20; Synonyms=ZCYTO10; ORFNames=UNQ852/PRO1801;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
```

RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21097717; PubMed=11163236; DOI=10.1016/S0092-8674(01)00187-8;
RA   Blumberg H., Conklin D., Xu W.F., Grossmann A., Brender T.,
RA   Carollo S., Eagan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,
RA   Jelinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,
RA   Prunkard D., Sexson S., Sprecher C., Waggie K., West J.,
RA   Whitmore T.E., Yao L., Kuechle M.K., Dale B.A., Chandrasekher Y.A.;
RT   "Interleukin 20: discovery, receptor identification, and role in
RT   epidermal function.";
RL   Cell 104:9-19(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA   Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA   Nickerson D.A.;
RT   "SeattleSNPs, NHLBI HL66682 program for genomic applications, UW-
RT   FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   PROTEIN SEQUENCE OF 25-39.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).

-!- FUNCTION: Cytokine that may be involved in epidermal function and
CC   psoriasis. Acts through STAT3.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed at very low levels in skin, trachea,
CC   and other tissues.
-!- SIMILARITY: Belongs to the IL-10 family.

DR   EMBL; AF224266; AAF36679.1; -; mRNA.
DR   EMBL; AF402002; AAK84423.1; -; Genomic_DNA.
DR   EMBL; AY358320; AAQ88686.1; -; mRNA.
DR   EMBL; BC069311; AAH69311.1; -; mRNA.
DR   EMBL; BC069364; AAH69364.1; -; mRNA.
DR   EMBL; BC069398; AAH69398.1; -; mRNA.
DR   EMBL; BC069425; AAH69425.1; -; mRNA.
DR   EMBL; BC069449; AAH69449.1; -; mRNA.
DR   EMBL; BC069487; AAH69487.1; -; mRNA.
DR   EMBL; BC069523; AAH69523.1; -; mRNA.
DR   EMBL; BC069559; AAH69559.1; -; mRNA.
DR   EMBL; BC074948; AAH74948.1; -; mRNA.
DR   EMBL; BC074949; AAH74949.1; -; mRNA.
DR   HSSP; Q9UHD0; 1N1F.
DR   HGNC; HGNC:6002; IL20.
DR   Ensembl; ENSG00000162891; Homo sapiens.
DR   MIM; 605619; -.
DR   InterPro; IPR012351; IL20.
DR   InterPro; IPR012352; IL-10_add_helix.
DR   InterPro; IPR000098; InterLeukin_10.
DR   Pfam; PF00726; IL10; 1.
DR   ProDom; PD003687; Interleukin_10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; 1.
DR   GO; GO:0005615; C:extracellular region; TAS.
DR   GO; GO:0005576; C:extracellular region; TAS.
DR   GO; GO:0045517; F:interleukin-20 receptor binding; TAS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0045506; P:positive regulation of epidermal cell diffe...; ISS.
DR   GO; GO:0045618; P:positive regulation of keratinocyte differe...; ISS.
DR   GO; GO:0042517; P:positive regulation of tyrosine phosphoryla...; TAS.
DR   GO; GO:0050727; P:regulation of inflammatory response; TAS.
KW   Cytokine; Direct protein sequencing; Signal.
FT   SIGNAL   1   24
FT   CHAIN   25   176   Interleukin-20.
FT   DISULFID   33   126   Potential.
FT   DISULFID   80   132   Potential.
FT   DISULFID   81   134   Potential.

FT   CONFLICT   48   48   B -> D (in Ref. 1).
FT   CONFLICT   126   126   C -> S (in Ref. 3).
SQ   SEQUENCE   176 AA; 20072 MW; 8385992500B6C447 CRC64;
Query Match   99.6%; Score 906; DB 1; Length 176;
Best Local Similarity   99.4%; Pred. No. 1.8e-80;
Matches 175; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MKASSLAFSLLSAAPYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
              |||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db   1 MKASSLAFSLLSAAPYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSEIRGSVQAKDGNI 60

Qy   61 DIRILRRTESLLQDTKPANCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120
              |||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db   61 DIRILRRTESLLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK 120

Qy   121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176

RESULT 2
IL20_MOUSE
ID   IL20_MOUSE   STANDARD;   PRT;   176 AA.
AC   Q9JKY9;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Interleukin-20 precursor (IL-20) (Four alpha helix cytokine ZCYTO10).
GN   Name=Il20; Synonyms=Zcyto10;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;

RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Skin;
RX   MEDLINE=21097717; PubMed=11163236; DOI=10.1016/S0092-8674(01)00187-8;
RA   Blumberg H., Conklin D., Xu W.F., Grossmann A., Brender T.,
RA   Carollo S., Eagan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,
RA   Jelinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,
RA   Prunkard D., Sexson S., Sprecher C., Waggie K., West J.,
RA   Whitmore T.E., Yao L., Kuechle M.K., Dale B.A., Chandrasekher Y.A.;
RT   "Interleukin 20: discovery, receptor identification, and role in
RT   epidermal function.";
RL   Cell 104:9-19(2001).

-!- FUNCTION: Cytokine that may be involved in epidermal function and
CC   psoriasis. Acts through STAT3.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-10 family.

DR   EMBL; AF224267; AAF36680.1; -; mRNA.
DR   HSSP; Q9UHD0; 1N1F.
DR   Ensembl; ENSMUSG00000026416; Mus musculus.
DR   MGI; MGI:1890473; Il20.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005576; C:extracellular region; TAS.
DR   GO; GO:0045517; F:interleukin-20 receptor binding; IDA.
DR   GO; GO:0030097; P:hemopoiesis; NAS.
DR   GO; GO:0045606; P:positive regulation of epidermal cell diffe...; ISS.
DR   GO; GO:0045618; P:positive regulation of keratinocyte differe...; ISS.
DR   GO; GO:0042517; P:positive regulation of tyrosine phosphoryla...; ISS.
DR   GO; GO:0050727; P:regulation of inflammatory response; ISS.
DR   InterPro; IPR012351; Cytokine_4_hlx.
DR   InterPro; IPR000098; InterLeukin_10.
DR   Pfam; PF00726; IL10; 1.
DR   ProDom; PD003687; Interleukin_10; 1.

DR   SMART; SM00188; IL10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; 1.
KW   Cytokine; Signal.
FT   SIGNAL   1   24   Potential.
FT   CHAIN   25   176   Interleukin-20.
FT   DISULFID   33   126   Potential.
FT   DISULFID   80   132   Potential.
FT   DISULFID   81   134   Potential.
SQ   SEQUENCE   176 AA; 20098 MW; 08577AF65657A771 CRC64;

Qy   Query Match   73.8%; Score 672; DB 1; Length 176;
     Best Local Similarity   75.3%; Pred. No. 1.5e-57;
     Matches 131; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

Qy   1 MKASSLAFSLLSAAPYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
           ||||||||||:|||||||||||||||||||||||||||||||:||||||||||||||||
Db   1 MKFGLAFGLFSAVGPFLLWTPLTGLKTLHLGSCVITANLQAIQKFSEIRDSVQABDTNI 60

Qy   61 DIRILRRTESLQDTKPANRCCLLRHLLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLIIK 120
           |||||||||:|:|||||||:|:||||||||||||:||||||||||||||||||||||||||
Db   61 DIRILRTTESLKDIKSLDRCCFLRHLVRFYLDRVFKVKVYQTPDHHTLRKISSLANSFLIIK 120

Qy   121 KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEE 174
           ||:|||||||||||||||||||||||||||:|||:||||:||||||||:||||
Db   121 KDLSVCHSHMACHCGEEAMEKYNQILSHPIELELQAAVVKALGELGILLRWMEE 174

RT   FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
DR   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG   Human chromosome 1 international sequencing consortium;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   PROTEIN SEQUENCE OF 25-39.
RA   Zhang Z., Henzel W.J.;
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF 19-177, AND DISULFIDE BONDS.
RX   PubMed=12403790; DOI=10.1074/jbc.M20860202200;
RA   Chang C., Magracheva E., Kozlov S., Fong S., Tobin G., Kotenko S.,
RA   Wlodawer A., Zdanov A.;
RT   "Crystal structure of interleukin-19 defines a new subfamily of
RT   helical cytokines.";
RL   J. Biol. Chem. 278:3308-3313(2003).
CC   -!- FUNCTION: May play some important roles in inflammatory responses.
CC   Up-regulates IL-6 and TNF-alpha and induces apoptosis (By
CC   similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-10 family.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; AF276915; AAG16755.1; -; Genomic_DNA.
DR   EMBL; AF453944; AAN40905.1; -; mRNA.
DR   EMBL; AF192498; AAF06663.1; -; mRNA.
DR   EMBL; AY040367; AAK91776.1; -; mRNA.
DR   EMBL; AF390905; AAK64499.1; -; Genomic_DNA.
DR   EMBL; AL049615; CAB72342.1; -; Genomic_DNA.
DR   PDB; 1N1F; X-ray; A=19-177.
DR   Pfam; PF00726; IL10; 1.
DR   InterPro; IPR012351; Cytokine_4_hlx.
DR   InterPro; IPR000098; Interleukin-10.
DR   SMART; SM00188; IL10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; 1.
DR   HGNC; HGNC:5990; IL19.
DR   Ensembl; ENSG00000142224; Homo sapiens.
DR   MIM; 605687; -.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0005125; F:cytokine activity; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   GO; GO:0007165; P:signal transduction; NAS.

KW   3D-structure; Apoptosis; Cytokine; Direct protein sequencing;
KW   Glycoprotein; Polymorphism; Signal.
FT   SIGNAL   1   24
FT   CHAIN   25   177   Interleukin-19.
FT   CARBOHYD   56   56   N-linked (GlcNAc...).
FT   CARBOHYD   135   135   N-linked (GlcNAc...).
FT   DISULFID   28   121   (Potential).
FT   DISULFID   75   127
FT   DISULFID   76   129
FT   VARIANT   175   175   S -> F.
FT   /FTId=VAR_013077.
SQ   SEQUENCE   177 AA; 20392 MW; 7CCFAC2217D8408 CRC64;

Qy   Query Match   37.1%; Score 337.5; DB 1; Length 177;
     Best Local Similarity   39.7%; Pred. No. 9.4e-25;
     Matches 69; Conservative 36; Mismatches 64; Indels 5; Gaps 1;

Qy   1 MKASSLAFSLLSAAPYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI 60
           |||||:|||::||||||||||:::|:::||||||||||||||:||||||||||||||||||
Db   1 MKLQCVSLWLLGTILILCSVDNHGLR-----RCLISTDMHIEESFQEIKRAIQAKDTFP 55

RESULT 3
ID   IL19_HUMAN   STANDARD;   PRT;   177 AA.
AC   Q9UHD0; Q9GR4; Q9NUA0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Interleukin-19 precursor (IL-19) (Melanoma differentiation associated
DE   protein-like protein) (NG.1).
GN   Name=IL19; Synonyms=ZMDA1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22577669; PubMed=12370360;
RA   Liao Y.-C., Liang W.G., Chen F.W., Hsu J.H., Yang J.J., Chang M.-S.;
RT   "IL-19 induces production of IL-6 and TNF-alpha and results in cell
RT   apoptosis through TNF-alpha.";
RL   J. Immunol. 169:4288-4297(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Conklin D., Petersen J., Loften-Day C., Whitmore T., Mucer M.,
RA   Sexson S., Smith D., Lok S., Powmder T., O'Hara P.;
RT   "Homo sapiens homolog of melanoma differentiation associated gene.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Kotenko S.V.;
RT   "Cloning, expression and initial characterization of interleukin-19
RT   (IL-19), a novel homolog of human interleukin-10 (IL-10).";
RL   Genes Immun. 1:442-450(2000).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Kotenko S.V., Peetka S.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT PHE-175.
RA   Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA   Nickerson D.A.;
RT   "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-

```
Qy   61  DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK  120
         |  :||||||  ::||||| ||:| :  |  :  |||||||||||||||| |||||||||
Db   56  NVTILSTLETLQIIKPLDVCCVTKNLLAFYVDRVPKDHQEPNPKILRKISSIANSFLYMQ  115

Qy  121  KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEE        174
         | |||| :|| |||| || ::   :  |  ||  ||||| ||||||| ||| |:
Db  116  KTLRQCEQROHCHRQEATNATRVIHDNYDQLEVHAAAIKSLGELDVFLAWINK        169
```

RESULT 4
```
ID   Q5VUT3_HUMAN    PRELIMINARY;     PRT;   215 AA.
AC   Q5VUT3;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Interleukin 19.
GN   Name=IL19; ORFNames=RP11-262N9.2-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kay M.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- -!- Genomic_DNA.
DR   EMBL; AL513315; CAH71814.1; -; Genomic_DNA.
DR   SMR; Q5VUT3; 60-215.
DR   Ensembl; ENSG00000142224; Homo sapiens.
DR   GO; GO:0005615; C:extracellular space; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR000098; Interleukin_10.
DR   Pfam; PF00726; IL10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; UNKNOWN_1.
KW   Cytokine.
SQ   SEQUENCE   215 AA;  24567 MW;  D79D6B0F11DA74E4 CRC64;
```

```
Query Match             37.1%;  Score 337.5;  DB 2;  Length 215;
Best Local Similarity   39.7%;  Pred. No. 1.2e-24;
Matches   69;  Conservative  36;  Mismatches  64;  Indels   5;  Gaps   1;
```

```
Qy    1  MKASSLAFSLLSAAFYILLWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNI   60
         ||  ::| ||| :: :| |  | :   | ||| ||          :  |   |||||| ::
Db   39  MKLQCVSLWLLGTIIILCSVDNHGLR------RCLISTDMHHIESPQEIKRAIQAKDTFP   93

Qy   61  DIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIK  120
         |  :||||||  ::||||| ||:| :  |  :  |||||||||||||||| |||||||||
Db   94  NVTILSTLETLQIIKPLDVCCVTKNLLAFYVDRVPKDHQEPNPKILRKISSIANSFLYMQ  153

Qy  121  KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEE       174
         | |||| :|| |||| || ::   :  |  ||  ||||| ||||||| ||| |:
Db  154  KTLRQCEQROHCHRQEATNATRVIHDNYDQLEVHAAAIKSLGELDVFLAWINK       207
```

RESULT 5
```
ID   Q4LDR4_BRARE    PRELIMINARY;     PRT;   168 AA.
AC   Q4LDR4;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Interleukin 10 family protein.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Euteleostomi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ram S., Daisuke I., Sakai M.;
RT   "Evolution of IL-10 family genes in teleosts.";
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB219579; BAE06181.1; -; mRNA.
SQ   SEQUENCE   168 AA;  19110 MW;  807D18AD736C709B CRC64;
```

```
Query Match             33.6%;  Score 306;  DB 2;  Length 168;
Best Local Similarity   42.4%;  Pred. No. 1.1e-21;
Matches   67;  Conservative  27;  Mismatches  58;  Indels   6;  Gaps   3;
```

```
Qy   76  PANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIKDLRLCHAHMTCHCG  135
         |  |  |: | : |  |  ||: ||| |||:| |||:|||||| |||:|||| | | ||
Db   10  LWDAAQG-RRLHLGSCKVNIHTHELRHHFQVRQGMISGDDHKGIRLLRKVDVMSSLQATE   68

Qy  136  EEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEE                      173
         |   ::  : :  | :   || | :| ||||| |  |:|
Db   69  ---SCCFLSQLLHFYWDTVFISYTSSHSLHRRTSVLANSFLISKDLRVCHANAHCECG   125
```

RESULT 6
```
ID   IL19_MOUSE      STANDARD;     PRT;   176 AA.
AC   Q8CJ70;
DT   10-MAY-2005 (Rel. 47, Created)
DT   10-MAY-2005 (Rel. 47, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Interleukin-19 precursor (IL-19).
GN   Name=Il19;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, AND FUNCTION.
     STRAIN=Swiss Webster / NIH;
     MEDLINE=22257669; PubMed=12370360;
RX   Liao Y.-C., Liang W.G., Chen F.W., Hsu J.H., Yang J.J., Chang M.-S.;
RT   "IL-19 induces production of IL-6 and TNF-alpha and results in cell
RT   apoptosis through TNF-alpha.";
RL   J. Immunol. 169:4288-4297(2002).
CC   -!- FUNCTION: May play some important roles in inflammatory responses.
CC       Up-regulates IL-6 and TNF-alpha and induces apoptosis.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-10 family.
CC   --------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------------
DR   EMBL; AF439945; AAN40905.1; -; mRNA.
DR   HSSP; Q9UHD0; 1N1F.
DR   SMR; Q8CJ70; 23-170.
DR   Ensembl; ENSMUSG00000016524; Mus musculus.
DR   MGI; MGI:1890472; Il19.
DR   GO; GO:0006917; P:induction of apoptosis; IDA.
DR   GO; GO:0042226; P:interleukin-6 biosynthesis; IDA.
DR   GO; GO:0006800; P:oxygen and reactive oxygen species metabolism; IDA.
DR   InterPro; IPR012351; Cytokine_4_hlx.
DR   InterPro; IPR000098; Interleukin_10.
DR   ProDom; PD003687; Interleukin_10.
DR   SMART; SM00188; IL10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; FALSE_NEG.
KW   Apoptosis; Cytokine; Glycoprotein; Signal.
FT   SIGNAL         1     24       Potential.
FT   CHAIN         25    176       Interleukin-19.
FT   CARBOHYD      56     56       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     127    127       N-linked (GlcNAc...) (Potential).
```

```
Qy   18  LWTPSTGLKTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNIDIRILRR--TESLQDTK   75
Db   10  LWDAAQG-RRLHLGSCKVNIHTHELRHHFQVRQGMISGDDHKGIRLLRKVDVMSSLQATE   68

Qy   76  PANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTIKDLRLCHAHMTCHCG  135
Db   69  ---SCCFLSQLLHFYWDTVFISYTSSHSLHRRTSVLANSFLISKDLRVCHANAHCECG  125

Qy  136  EEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEE                      173
Db  126  ENTRLQLKSIQTAYEKLDQAAGTVKAIGELDSLLEWIE                       163
```

```
FT   CARBOHYD    134    134    N-linked (GlcNAc...) (potential).
FT   DISULFID     28    120    By similarity.
FT   DISULFID     74    126    By similarity.
FT   DISULFID     75    128    By similarity.
SQ   SEQUENCE   176 AA;  20288 MW;  73B6C1BC54077FDC CRC64;

Qy   Query Match
Best Local Similarity   30.9%;
Matches   56;  Conservative  35;  Mismatches  53;  Indels  1;  Gaps  1;

Qy    29  NLGSCVIATNLQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLR   88
          |.|| ||.:.|::|:..::||:.:|||| :|...::||:..|.:|:|||.:|||||| :|
Db    24  SLRRCLISVDMRLIEKSFHEIKRAMQTKDFFKNVTIL-SLENLRSIKPGDVCCMTNNLLT   82

Qy    89  LYLDRVFKNYQTPDHYTLRKISSLANSFLTIKKDLRLCHAHMTCHGEEAMKKYSQILSH   148
          |||||||||||| ....:::||.|||.::...||||||||||||| :|:|| ||||:|:.
Db    83  FYRDRVFQDHQERSLEVLRRISSIANSFLCVQKSLERCQVHRQCNCSQEATNATRIIHDN  142

Qy   149  FEKLEPQAVVKALGELDILLQWME  173
          ||||||||||||||||||||||||
Db   143  YNQLEVSSAALKSLGELNILLAWID  167
```

```
RESULT 7
Q7SX60_TETNG

AC   Q7SX60;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Interleukin-20.
GN   Name=IL20;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetraodontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=12869211; DOI=10.1186/1471-2164-4-29;
RA   Lufalla G., Crollius H.R., Stange-Thomann N., Jaillon O.,
RA   Mogensen K., Monneron D.;
RT   "Comparative genomic analysis reveals independent expansion of a
RT   lineage-specific gene family in vertebrates: The class II cytokine
RT   receptors and their ligands in mammals and fish.";
RL   BMC Genomics 4:29-29(2003).
DR   EMBL; AY294557; AAP57414.1; -; Genomic_DNA.
DR   EMBL; AY294558; AAP57416.1; -; mRNA.
DR   GO; GO:0005615; C:extracellular space; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR012351; Cytokine_4_hlx.
DR   InterPro; IPR000098; Interleukin_10.
DR   Pfam; PF00726; IL10; 1.
DR   ProDom; PD003687; Interleukin_10; 1.
DR   SMART; SM00188; IL10; 1.
SQ   SEQUENCE   175 AA;  19838 MW;  DE6FA67E0038E034 CRC64;

Qy   Query Match
Best Local Similarity   29.3%;  Pred. No. 8.4e-18;
Matches   57;  Conservative  33;  Mismatches  53;  Indels  7;  Gaps  3;

Qy    26  KTLNLGSCVIATNLQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQD            85
Db    24  QTLLVDSCISADLQEMHQHSNIRLNAITEDEEIGVKLLSK-RLMEDVQDGQRCCFLRL    82

Qy    86  LLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTI--KKDLRLCHAHMTCHGEEAMKKYS  143
Db    83  VLQPYIDKVFPSYLSSHPQNQSSSSLANTFIIIVRKQMIQKCH---CLCEQTQKKVD   138

Qy   144  QILSHFEKLEPQAVVKALGELDILLQWME  173
```

```
Db   139  SLLDAFNKLEASKAVLKAVGELDTVLQWLQ  168

RESULT 8
Q92SJ3_MOUSE

ID   Q92SJ3_MOUSE  PRELIMINARY;  PRT;  220 AA.
AC   Q92SJ3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Th2-specific cytokine FISP.
GN   Name=I124;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BALB/c;
RX   MEDLINE=21240641; PubMed=11342597;
RA   Schaefer G., Venkataraman C., Schindler U.;
RT   "FISP (IL-4-induced secreted protein), a novel cytokine-like molecule
RT   secreted by Th2 cells.";
RL   J. Immunol. 166:5859-5863(2001).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; AF333251; AAK52470.1; -; mRNA.
DR   Ensembl; ENSMUSG00000026420; Mus musculus.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR000098; Interleukin_10.
DR   ProDom; PD003687; Interleukin_10; 1.
DR   SMART; SM00188; IL10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; 1.
KW   Cytokine.
SQ   SEQUENCE   220 AA;  25168 MW;  5BF76C8612AC909D CRC64;

Qy   Query Match
Best Local Similarity   24.4%;  Pred. No. 2.6e-13;
Matches   56;  Conservative  30;  Mismatches  71;  Indels  6;  Gaps  4;

Qy    17  LLWTPSTGL--KTLNLGSC-VIATNLQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQD   73
Db    55  LLWNQVPGLEGGQBRFGSCQVTGVVLPELWEARFWTVKNTVQDDITSIRLL-KPQVLRN   113

Qy    74  TKPANRCCLLRHLLRLYLDRVFKNYQT--PDHYTLRKISSLANSFLTIKKDLRLCHAHMT  131
Db   114  VSGAESCYLAHSLLKFYLNTVFKNYHSKIAKFKVLRSFSTLANNFIVIMSQLQPSKDNSM  173

Qy   132  CHGEEAMKKYSQILSHFEKLEPQAVVKALGELDILLQWMEE  174
Db   174  LPISESAHQRFLLFRRAFKQLDTEVALVKAFGEVDILLTWMQK  216

RESULT 9
Q92SE4_MOUSE

ID   Q92SE4_MOUSE  PRELIMINARY;  PRT;  181 AA.
AC   Q92SE4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Melanoma differentiation associated gene-7.
GN   Name=I124;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129/SvJ;
RA   Madireddi M.T., Lin J., Su Z., Shay J.W., Huberman E., Fisher P.B.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
```

```
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; AF235006; AAK52590.1; -; mRNA.
DR   Ensembl; ENSMUSG00000026420; Mus musculus.
DR   MGI; MGI:2135548; Il24.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR000098; Interleukin_10.
DR   ProDom; PD003687; Interleukin_10; 1.
DR   SMART; SM00188; IL10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; 1.
KW   Cytokine.
SQ   SEQUENCE   181 AA;  20812 MW;  05CA43872D53D555 CRC64;

Qy   Query Match     24.2%;   Score 220;   DB 2;   Length 181;
Best Local Similarity   34.4%;   Pred. No. 3.2e-13;
Matches   56;   Conservative   30;   Mismatches 71;   Indels   6;   Gaps   4;

Qy   17 LLWTPSTGL--KTLNLGSC-VIATNLQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQD 73
           |||  |  :   |:|| |||  |    |||:   | ||  || ||| ||| :|||||||||| ||
Db   16 LLWNQVPGLLEGQEFRSGSCQVTGVVLPELWEAFWTVKNTVQTQDDITSIRLL-KPQVLRN 74

Qy   74 TKPANRCCLLRHLLRLYLDRVFKNYQT--PDHYTLRKISSLANSPLTIIKKDLRLCHAHMT 131
           |||||  ||  | |||:|  ||:|:|||:| ||:|||   |  | :| ||    | |||| |
Db   75 VSGAESCYLAHSLLKFYLNTVFKNYHSKIAKFKVLRSFSTLANNFIVIMSQLQPSKDNSM 134

Qy  132 CHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEE 174
           |       |   :|:   | |:     :   | |: |:|| ||:|| : |:
Db  135 LPISSAHQRFLLFRRAFKQLDTEVALVKAFGEVDILLTWMQK 177
```

RESULT 10
IL24_HUMAN

```
ID   IL24_HUMAN     STANDARD;      PRT;   206 AA.
AC   Q13007; Q96DB0; Q96KG4;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Interleukin-24 precursor (Suppression of tumorigenicity 16 protein)
DE   (Melanoma differentiation-associated protein 7) (MDA-7)
GN   Name=IL24; Synonyms=MDA7, ST16;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Melanoma;
RX   MEDLINE=96132699; PubMed=8545104;
RA   Jiang H., Lin J.J., Su Z.-Z., Goldstein N.I., Fisher P.B.;
RT   "Subtraction hybridization identifies a novel melanoma differentiation
RT   associated gene, mda-7, modulated during human melanoma
RT   differentiation, growth and progression.";
RL   Oncogene 11:2477-2486(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE, AND VARIANT HIS-124.
RC   TISSUE=Fibroblast;
RA   Madireddi M.T., Lin J.J., Su Z.-Z., Shay J.W., Huberman E., Fisher P.B.;
RT   "Genomic structure, chromosomal localization and expression of
RT   melanoma differentiation associated gene-7 (mda-7): potential
RT   relationship with cellular senescence.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS HIS-124, ARG-125 AND
RP   LEU-131.
RA   Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA   Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT   "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT   FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Peat J., Kube D., Eskdale J., Jueliger S., Gallagher G.;
RT   "The human MDA-7 gene.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   PROTEIN SEQUENCE OF 52-66.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [7]
RP   CHARACTERIZATION.
RX   MEDLINE=99045696; PubMed=9826712; DOI=10.1073/pnas.95.24.14400;
RA   Su Z.-Z., Madireddi M.T., Lin J.J., Young C.S.H., Kitada S.,
RA   Reed J.C., Goldstein N.I., Fisher P.B.;
RT   "The cancer growth suppressor gene mda-7 selectively induces apoptosis
RT   in human breast cancer cells and inhibits tumor growth in nude mice.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:14400-14405(1998).
CC   -!- FUNCTION: Has antiproliferative properties in human melanoma cells
CC       and may contribute to terminal cell differentiation. May also
CC       function as a negative regulator of melanoma progression.
CC       Formation in vivo in nude mice. They found that it selectively
CC       induces apoptosis in human breast cancer cells.
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- TISSUE SPECIFICITY: Up-regulated in melanoma cells induced to
CC       terminally differentiate.
CC   -!- SIMILARITY: Belongs to the IL-10 family.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; U16261; AAA91780.1; -; mRNA.
DR   EMBL; AF276916; AAG41401.1; -; Genomic_DNA.
DR   EMBL; AF235005; AAK52589.1; -; Genomic_DNA.
DR   EMBL; AY062931; AAL34146.1; -; Genomic_DNA.
DR   EMBL; BC009681; AAH09681.1; -; mRNA.
DR   Ensembl; ENSG00000162892; Homo sapiens.
DR   HGNC; HGNC:11346; IL24.
DR   H-InvDB; HIX0001532; -.
DR   MIM; 604136; -.
DR   GO; GO:0006915; P:apoptosis; TAS.
DR   InterPro; IPR012351; Cytokine_4_hlx.
DR   InterPro; IPR000098; Interleukin_10.
DR   ProDom; PD003687; Interleukin_10; 1.
DR   SMART; SM00188; IL10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; 1.
KW   Apoptosis; Cytokine; Direct protein sequencing; Glycoprotein;
KW   Polymorphism; Signal.
```

```
FT   SIGNAL          1     51                Interleukin-24.
FT   CHAIN          52    206
FT   CARBOHYD       85     85                N-linked (GlcNAc...)   (Potential).
FT   CARBOHYD       99     99                N-linked (GlcNAc...)   (Potential).
FT   CARBOHYD      126    126                N-linked (GlcNAc...)   (Potential).
FT   CARBOHYD      124    124                N-linked (GlcNAc...)   (Potential).
FT   VARIANT       125    125                Y -> H (in dbSNP:11502258).
FT   VARIANT       124    124                Y -> R (in dbSNP:3093431).
FT                                           /FTId=VAR_011974.
FT   VARIANT       131    131                V -> L (in dbSNP:30934446).
FT                                           /FTId=VAR_013097.
FT   CONFLICT       14     14                A -> AS (In Ref. 4).
FT                                           /FTId=VAR_013098.
SQ   SEQUENCE      206 AA;  23825 MW;  CB8135083EAB8DDD CRC64;
```

```
Query Match             23.8%;  Score 217;  DB 1;  Length 206;
Best Local Similarity   32.8%;  Pred. No. 7.3e-13;
Matches    57;  Conservative    39;  Mismatches   66;  Indels   12;  Gaps    5;

Qy      6  LAFSLLSAAFYLLWTPSTGL--KTLNLGSCVIATNL-QEIRNGFSDIRGSVQAKDGNIDI  62
           |||:|      ||:|  |  ::| |::|: :|||  |||
Db     36  LGFTL------LLWSQVSGAQGQEFHFGPCQVKGVVPQKLWEAFWAVKDTMQAQDNITSA  89

Qy     63  RILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNY--QTPDHYTLRKISSLANSFLTIK  120
Db     90  RLLQQ-EVLQNVSDAESCYLVHTLLEFYLKTVFKNYHNRTVEVRTLKSFSTLANNFVLIV  148

Qy    121  KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEE  174
Db    149  SOLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAALTKALGEVDILLTWMQK  202
```

RESULT 11
Q53X27_HUMAN

ID   Q53X27_HUMAN PRELIMINARY; PRT; 207 AA.
AC   Q53X27;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Interleukin 24.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; BT007156; AAP35820.1; -; mRNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
KW   Cytokine.
SQ   SEQUENCE   207 AA; 23912 MW; 17687A467B9CB551 CRC64;

```
Query Match             23.8%;  Score 217;  DB 2;  Length 207;
Best Local Similarity   32.8%;  Pred. No. 7.4e-13;
Matches    57;  Conservative    39;  Mismatches   66;  Indels   12;  Gaps    5;

Qy      6  LAFSLLSAAFYLLWTPSTGL--KTLNLGSCVIATNL-QEIRNGFSDIRGSVQAKDGNIDI  62
           |||:|      ||:|  |  ::| |::|: :|||  |||
Db     37  LGFTL------LLWSQVSGAQGQEFHFGPCQVKGVVPQKLWEAFWAVKDTMQAQDNITSA  90

Qy     63  RILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNY--QTPDHYTLRKISSLANSFLTIK  120
Db     91  RLLQQ-EVLQNVSDAESCYLVHTLLEFYLKTVFKNYHNRTVEVRTLKSFSTLANNFVLIV  149

Qy    121  KDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEE  174
Db    150  SOLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAALTKALGEVDILLTWMQK  203
```

RESULT 12
MOB5_RAT

ID   MOB5_RAT STANDARD; PRT; 183 AA.
AC   Q9JI24;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Cytokine-like protein Mob-5 precursor.
GN   Name=Mob5;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20387329; PubMed=10825166; DOI=10.1074/jbc.M001958200;
RA   Zhang R., Tan Z., Liang P.;
RT   "Identification of a novel ligand-receptor pair constitutively
RT   activated by ras oncogenes.";
RL   J. Biol. Chem. 275:24436-24443(2000).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-10 family.

DR   EMBL; AF269251; AAF75553.1; -; mRNA.
DR   Ensembl; ENSRNOG00000004470; Rattus norvegicus.
DR   GO; GO:0048014; P:fibroblast proliferation; TAS.
DR   GO; GO:0042060; P:wound healing; TAS.
DR   InterPro; IPR012351; Cytokine_4_hlx.
DR   InterPro; IPR000098; Interleukin-10.
DR   ProDom; PD003687; Interleukin-10_1.
DR   SMART; SM00188; IL10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; 1.
KW   Cytokine; Glycoprotein; Signal.
FT   SIGNAL   1   28   Potential.
FT   CHAIN   29   183   Cytokine-like protein Mob-5.
FT   CARBOHYD   76   76   N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   183 AA; 21096 MW; AF7A11466C491AC4 CRC64;

```
Query Match             21.0%;  Score 191;  DB 1;  Length 183;
Best Local Similarity   33.1%;  Pred. No. 2.2e-10;
Matches    49;  Conservative    31;  Mismatches   60;  Indels    8;  Gaps    5;

Qy     31  GSC-VIATNL-QEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLRL  89
           | : |::|:  |:||||||||||||||||:||:||:|| :::|
Db     34  GPCQVGVLPELWEAFWTKVKNTVKTQDELTSVRLL-KPQVLQNVSDAESCYLAHSLLKF  92

Qy     90  YLDRVFKNYQTP--DHYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILS  147
Db     93  YLNTVFKNYHSKIVKFKVLKSFSTLANNFLVIMSKLQPSKDNAMLPISDSARRF--LIY  150

Qy    148  H--FEKLEPQAAVVKALGELDILLQWMEE  173
Db    151  HRTFKQLDIEVALAKAFGEVDILLAWMQ  178
```

RESULT 13
Q9WP8_RAT

ID   Q9WP8_RAT PRELIMINARY; PRT; 183 AA.
AC   Q9WP8;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

```
DE   C49a.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=99308986; PubMed=10381256;
RX   DOI=10.1002/(SICI)1097-4644(19990701)74:1<1:1:AID-JCB1>3.3.CO;2-D;
RA   Soo C., Shaw W.W., Freymiller E., Longaker M.T., Bertolami C.N.,
RA   Chiu R., Tieu A., Ting K.;
RT   "Cutaneous rat wounds express c49a, a novel gene with homology to the
RT   human melanoma differentiation associated gene, mda-7.";
RL   J. Cell. Biochem. 74:1-10(1999).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; AF004774; AAB69171.1; -; mRNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR000098; Interleukin-10.
DR   ProDom; PD003687; Interleukin_10; 1.
DR   PROSITE; PS00520; INTERLEUKIN_10; 1.
KW   Cytokine.
SQ   SEQUENCE  183 AA;  21052 MW;  F69A96AFC473E4F CRC64;

Query Match             20.5%;  Score 187;  DB 2;  Length 183;
Best Local Similarity   32.2%;
Matches   47;  Conservative   29;  Mismatches   66;  Indels    4;  Gaps    3;

Qy         31 GSC-VIATNLQEIRNGFSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRL 89
                 |||  ||| : : ||: ||| :: || : ||: : |: |||||| :|||||||
Db         34 GPCQVTGVLLPELWEAFWTVKNTVKTQDELTSARLL-KPQVLQNVSDAESCYLAHSLLKF 92

Qy         90 YLDRVFKNYQTP--DHYTLRKISSLANSFLTIKDLRLRLCHAHMTCHCGEEAMKKYSQILS 147
                 |||| || : ||| |||||||||||||||: : || | : ||| ::|
Db         93 YLNTVFKNYHSKIVKFKVLKSFSTLANNFLVIMSKLQPSKDNAMLPISDSARRRFLLFHR 152

Qy        148 HFEKLEPQAAVVKALGELDILLQWME 173
               | | ||| : |||| ||| :|:
Db        153 TFKQLDIEVALAKAFGEVDILLAWMQ 178
```

```
RESULT 14
ID   Q6A2H5_CHICK PRELIMINARY;    PRT;   175 AA.
AC   Q6A2H5;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Interleukin-10.
GN   Name=IL-10;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Rothwell L., Young J., Zoorob R., Whittaker C.A., Hesketh P.,
RA   Archer A., Smith A.L., Kaiser P.;
RT   "Cloning and Characterization of Chicken IL-10 and Its Role in the
RT   Immune Response to Eimeria maxima.";
RL   J. Immunol. 173:2675-2682(2004).
DR   EMBL; AJ621254; CAF18432.1; -; mRNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR012351; Cytokine_4_hlx.
DR   InterPro; IPR012352; IL-10_add_helix.
DR   InterPro; IPR000098; Interleukin-10.
DR   Pfam; PF00726; IL10; 1.
DR   PRINTS; PR01294; INTRLEUKIN10.
DR   ProDom; PD003687; Interleukin_10; 1.
DR   SMART; SM00188; IL10; 1.
SQ   SEQUENCE  175 AA;  20514 MW;  B0966EBEAFDFB050 CRC64;

Query Match             19.3%;  Score 175.5;  DB 2;  Length 175;
Best Local Similarity   30.3%;  Pred. No. 7e-09;
Matches   53;  Conservative   32;  Mismatches   81;  Indels    9;  Gaps    5;

Qy          1 MKASSLAFSLLLSAAFYLLWTPSTGLKTLNLG-SCVIATNLQEIRNGFSDIRGSVQAKDGN 59
                |||:  ||| ::| :  |  ::|| | :||| :  :| |||||||||||||||:||||||
Db          1 MQTCCOALLLLLAACTL---PAHCLEPTCLHFSELLPARLRELRVKFEEIKDYFQSRDDE 57

Qy         60 IDIRILRRTESLQDTKPANRCCLLRHLLRLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTI 119
              |||||||||||||||||||||||||||:  : ||  : | : ||| ::| |||||||||||
Db         58 LNIQLL-SSELLDEFKGTFGCCQSVSEMLRFYTDEVLPRAMQTSTSHQQSMGDLGNMLLGL 116

Qy        120 KKDLRLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEE 174
              | : |||| : |||| ::|  :||  ||: : :  |::|  |||  ||| :|:
Db        117 KATMRRCHRFFTC---EKRSKAIKQIKETFEKMD-ENGIYXAMGEFDIFINYIEE 167
```

```
RESULT 15
ID   Q6A2H4_CHICK PRELIMINARY;    PRT;   175 AA.
AC   Q6A2H4;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Interleukin-10.
GN   Name=IL10;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Rothwell L., Young J., Zoorob R., Whittaker C.A., Hesketh P.,
RA   Archer A., Smith A.L., Kaiser P.;
RT   "Cloning and Characterization of Chicken IL-10 and Its Role in the
RT   Immune Response to Eimeria maxima.";
RL   J. Immunol. 173:2675-2682(2004).
DR   EMBL; AJ621614; CAF21727.1; -; Genomic_DNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR012351; Cytokine_4_hlx.
DR   InterPro; IPR012352; IL-10_add_helix.
DR   InterPro; IPR000098; Interleukin-10.
DR   Pfam; PF00726; IL10; 1.
DR   PRINTS; PR01294; INTRLEUKIN10.
DR   ProDom; PD003687; Interleukin_10; 1.
DR   SMART; SM00188; IL10; 1.
SQ   SEQUENCE  175 AA;  20496 MW;  A4966ABAAFDFB057 CRC64;

Query Match             19.3%;  Score 175.5;  DB 2;  Length 175;
Best Local Similarity   30.3%;  Pred. No. 7e-09;
Matches   53;  Conservative   32;  Mismatches   81;  Indels    9;  Gaps    5;

Qy          1 MKASSLAFSLLLSAAFYLLWTPSTGLKTLNLG-SCVIATNLQEIRNGFSDIRGSVQAKDGN 59
                |||:  ||| ::| :  |  ::|| | :||| :  :| |||||||||||||||:||||||
Db          1 MQTCCOALLLLLAACTL---PAHCLEPTCLHFSELLPARLRELRVKFEEIKDYFQSRDDE 57

Qy         60 IDIRILRRTESLQDTKPANRCCLLRHLLRLRLYLDRVFKNYQTPDHYTLRKISSLANSFLTI 119
              |||||||||||||||||||||||||||:  : ||  : | : ||| ::| |||||||||||
Db         58 LNIQLL-SSELLDEFKGTFGCCQSVSEMLRFYTDEVLPRAMQTSTSHQQSMGDLGNMLLGL 116

Qy        120 KKDLRLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEE 174
              | : |||| : |||| ::|  :||  ||: : :  |::|  |||  ||| :|:
Db        117 KATIRCHRFFTC---EKRSKAIKQIKETFEKMD-ENGIYXAMGEFDIFINYIEE 167
```

OM protein - nucleic search, using frame_plus_p2n model.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: December 28, 2005, 11:43:57 ; Search time 2945 Seconds
(without alignments)
2779.442 Million cell updates/sec

Title: US-10-789-251-26
Perfect score: 753
Sequence: 1 CVIATNLQEIRNGFSDIRGS.........AVVKALGELDILLQWMEETE 144

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 2842172553 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV=xlp
-MODEL=frame+_p2n.model
-O=/cgn2_1/USPTO_spool_p/US10789251/runat_23122005_152435_19747/app_query.fasta_1.327
-Db=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000000
-USER=US10789251@CGN_1_1_7415 @runat_23122005_152435_19747 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_om:*
4: gb_env:*
5: gb_ov:*
6: gb_om:*
7: gb_pat:*
8: gb_ph:*
9: gb_pr:*
10: gb_ro:*
11: gb_rss:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: gb_htg:*
16: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	753	100.0	926	6	BD087297	BD087297 Mammalian
2	753	100.0	926	6	CQ818183	CQ818183 Sequence
3	753	100.0	926	6	CS109174	CS109174 Sequence

4	753	100.0	926	6	CS110179	CS110179 Sequence
5	753	100.0	926	6	AR342856	AR342856 Sequence
6	753	100.0	926	8	AF224266	AF224266 Homo sapi
7	749	99.5	462	6	CS123418	CS123418 Sequence
8	749	99.5	531	6	CS123418	CS123418 Sequence
9	749	99.5	531	8	BC069311	BC069311 Homo sapi
10	749	99.5	531	8	BC069364	BC069364 Homo sapi
11	749	99.5	531	8	BC069398	BC069398 Homo sapi
12	749	99.5	531	8	BC069425	BC069425 Homo sapi
13	749	99.5	531	8	BC069449	BC069449 Homo sapi
14	749	99.5	531	8	BC069487	BC069487 Homo sapi
15	749	99.5	531	8	BC069523	BC069523 Homo sapi
16	749	99.5	531	8	BC069559	BC069559 Homo sapi
17	749	99.5	531	11	AY893295	AY893295 Synthetic
18	749	99.5	531	11	AY885562	AY885562 Synthetic
19	749	99.5	603	8	AY891211	AY891211 Synthetic
20	749	99.5	603	8	BC074948	BC074948 Homo sapi
21	749	99.5	867	6	BC074949	BC074949 Homo sapi
22	749	99.5	867	6	AX498605	AX498605 Sequence
23	746	99.1	926	6	AX537938	AX537938 Sequence
24	746	99.1	926	6	CQ889881	CQ889881 Sequence
25	739	98.1	1571	6	CQ889943	CQ889943 Sequence
26	739	98.1	1571	6	CQ970652	CQ970652 Sequence
27	739	98.1	1571	6	CS133455	CS133455 Sequence
28	739	98.1	1571	6	AX092406	AX092406 Sequence
29	739	98.1	1571	6	AX358964	AX358964 Sequence
30	739	98.1	1571	6	AX362457	AX362457 Sequence
31	739	98.1	1571	6	AX376542	AX376542 Sequence
32	739	98.1	1571	6	AX454700	AX454700 Sequence
33	739	98.1	1571	6	AX463964	AX463964 Sequence
34	739	98.1	1571	6	AX464412	AX464412 Sequence
35	739	98.1	1571	6	AX491178	AX491178 Sequence
36	739	98.1	1571	8	AX697333	AX697333 Homo sapi
37	739	98.1	1571	8	AY358320	AY358320 Homo sapi
38	686	91.1	747	6	CQ818192	CQ818192 Mammalian
39	686	91.1	747	6	CS109203	CS109203 Sequence
40	686	91.1	747	6	CS112208	CS112208 Sequence
41	686	91.1	747	6	AR342863	AR342863 Sequence
42	587.5	78.0	793	6	BD087298	BD087298 Mammalian
43	587.5	78.0	793	6	CQ818185	CQ818185 Sequence
44	587.5	78.0	793	6	CS109177	CS109177 Sequence
45	587.5	78.0	793	6	CS110182	CS110182 Sequence

ALIGNMENTS

RESULT 1
BD087297

LOCUS   BD087297   926 bp   DNA   linear   PAT 27-AUG-2002
DEFINITION   Mammalian cytokine-like polypeptide-10.
ACCESSION   BD087297
VERSION   BD087297.1   GI:22632907
KEYWORDS   JP 2001524313-A/1.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1 (bases 1 to 926)
AUTHORS   Conklin,D.C., Haldeman,B.A. and Grossmann,A.
TITLE   Mammalian cytokine-like polypeptide-10
JOURNAL   Patent: JP 2001524313-A 1 04-DEC-2001;
ZYMOGENETICS INC
COMMENT   OS   Homo sapiens (human)
PN   JP 2001524313-A/1
PD   04-DEC-2001
PF   25-NOV-1998 JP 2000522245
PR   26-NOV-1997 US 08/979156
PI   DARRELL C CONKLIN, BETTY A HALDEMAN, ANGELIKA GROSSMANN PC
PC   C12N15/09,A01K67/027,A61K38/00,A61K48/00,A61P1/02,A61P11/00, PC
PC   A61P17/00,
PC   A61P35/00,A61P37/02,A61P43/00,C07K14/52,C07K16/24,C07K16/42,
PC   C12N15/00,

FEATURES

```
           PC    A61K37/02
           CC    Mammalian cytokine-like polypeptide-10
           FH    Key                 Location/Qualifiers
           FT    CDS                 (45)..(572)

     source        1..926
                   /organism="Homo sapiens"
                   /mol_type="genomic DNA"
                   /db_xref="taxon:9606"

ORIGIN
```

Alignment Scores:

```
Pred. No.:
Score:                  3.22e-72     Length:            926
Percent Similarity:     753.00       Matches:           144
Best Local Similarity:  100.00%      Conservative:        0
Query Match:            100.00%      Mismatches:          0
DB:                     6            Indels:              0
                                     Gaps:                0
```

US-10-789-251-26 (1-144) x BD087297 (1-926)

```
Qy    1 CysValIleAlaThrAsnLeuGlnGluIleLeuArgAsnGlyPheSerAspIleArgGlySer 20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACAATACGGGGGCAGT 200

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260

Qy   41 AspThrLysProAlaAsnArgCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261 GACACAAAAGCCTGCGAATCGAATCGGTCCTCCTGCGCCATTTGCTAAGACTCTATCTGGAC 320

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy   81 AlaAsnSerPheLeuThrIleLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440

Qy  101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  441 CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

Qy  121 GluProGlnAlaAlaValValLysAlaIleGlyGluLeuAspIleLeuLeuGlnTrpMet 140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  501 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 560

Qy  141 GluGluThrGlu 144
          ||||||||||||
Db  561 GAGGAGACAGAA 572
```

```
RESULT 2
LOCUS       CQ818183     926 bp    DNA    linear    PAT 07-JUN-2004
DEFINITION  Sequence 1 from Patent EP1424393.
ACCESSION   CQ818183
VERSION     CQ818183.1  GI:48426975
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Conklin,D.C., Haldeman,B.A., and Grossmann,A.
  TITLE     Mammalian cytokine-like polypeptide-10
  JOURNAL   Patent: EP 1424393-A1 02-JUN-2004;
            Zymogenetics Inc (US)
FEATURES             Location/Qualifiers
     source          1..926
                     /organism="Homo sapiens"
```

```
           CDS             /mol_type="unassigned DNA"
                           /db_xref="taxon:9606"
                           45..575
                           /note="unnamed protein product"
                           /codon_start=1
                           /protein_id="CAG33976.1"
                           /db_xref="GI:48426976"
                           /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRN
                           GFSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQFPD
                           HYTLRKISSLANSFLTIKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVK
                           AIGELDILLQWMETE"

ORIGIN
```

Alignment Scores:

```
Pred. No.:
Score:                  3.22e-72     Length:            926
Percent Similarity:     753.00       Matches:           144
Best Local Similarity:  100.00%      Conservative:        0
Query Match:            100.00%      Mismatches:          0
DB:                     6            Indels:              0
                                     Gaps:                0
```

US-10-789-251-26 (1-144) x CQ818183 (1-926)

```
Qy    1 CysValIleAlaThrAsnLeuGlnGluIleLeuArgAsnGlyPheSerAspIleArgGlySer 20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACAATACGGGGGCAGT 200

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260

Qy   41 AspThrLysProAlaAsnArgCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261 GACACAAAAGCCTGCGAATCGAATCGGTCCTCCTGCGCCATTTGCTAAGACTCTATCTGGAC 320

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy   81 AlaAsnSerPheLeuThrIleLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440

Qy  101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  441 CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

Qy  121 GluProGlnAlaAlaValValLysAlaIleGlyGluLeuAspIleLeuLeuGlnTrpMet 140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  501 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 560

Qy  141 GluGluThrGlu 144
          ||||||||||||
Db  561 GAGGAGACAGAA 572
```

```
RESULT 3
LOCUS       CS109174     926 bp    DNA    linear    PAT 22-JUN-2005
DEFINITION  Sequence 1 from Patent WO2005052001.
ACCESSION   CS109174
VERSION     CS109174.1  GI:68148023
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xu,W., Kindsvogel,W.R., Chen,Z., Hughes,S.D., Chandrasekher,Y.A.,
            Dillon,S.R., Lehner,J.M., Siadak,A.W., Sivakumar,P.V. and
            Moore,M.D.
  TITLE     Anti-il-20 receptor antibodies and binding partners and methods of
            using in inflammation
```

(Left column)

```
JOURNAL     Patent: WO 200505200I-A 1 09-JUN-2005;
            ZymoGenetics, Inc. (US)
            1. .926
FEATURES    Location/Qualifiers
  source    1. .926
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
  CDS       45..575
            /codon_start=1
            /db_xref="GI:68148024"
            /protein_id="CAJ09892.1"
            /note="unnamed protein product"
            /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRN
            GFSDIRGSVQAKDGNIDIRLILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPD
            HYTLRKISSLANSFLTIKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVK
            ALGELDILLQWMEETE"

ORIGIN
Alignment Scores:
Pred. No.:
Score:                      3.22e-72        Length:         926
Percent Similarity:         753.00          Matches:        144
Best Local Similarity:      100.00%         Conservative:   0
Query Match:                100.00%         Mismatches:     0
DB:                         6               Indels:         0
                                            Gaps:           0

US-10-789-251-26 (1-144) x CS109174 (1-926)

Qy    1  CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer  20
Db  141  TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGGCAGT  200

Qy   21  ValGlnAlaLysAspGlyAsnIleAspIleArgLeuIleLeuArgArgThrGluSerLeuGln  40
Db  201  GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA  260

Qy   41  AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp  60
Db  261  GACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGAC  320

Qy   61  ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu  80
Db  321  AGGGTATTTAAAAACTACCAGACACCCCTGACCATTATACTCTCCCGGAAGATCAGCAGCCTC  380

Qy   81  AlaAsnSerPheLeuThrIleLysAspLeuArgLeuCysHisAlaHisMetThrCys  100
Db  381  GCCAATTCCTTTACCATCAAGGAGGACCTTCGGCTCTGTCATGCCCACATGACATGC  440

Qy  101  HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu  120
Db  441  CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  500

Qy  121  GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet  140
Db  501  GAACCTCAGCCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG  560

Qy  141  GluGluThrGlu  144
Db  561  GAGGAGACAGAA  572
```

(Right column)

```
AUTHORS     Xu,W., Kindsvogel,W.R., Chen,Z., Hughes,S.D., Chandrasekher,Y.A.,
            Dillon,S.R., Lehner,J.M., Siadak,A.W., Sivakumar,P.V. and
            Moore,M.D.
TITLE       Anti-il-20 antibodies and binding partners and methods of using in
            inflammation
JOURNAL     Patent: WO 200505200-A 1 09-JUN-2005;
            ZymoGenetics, Inc. (US)
            1. .926
FEATURES    Location/Qualifiers
  source    1. .926
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
  CDS       45..575
            /codon_start=1
            /db_xref="GI:68148438"
            /protein_id="CAJ09906.1"
            /note="unnamed protein product"
            /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRN
            GFSDIRGSVQAKDGNIDIRLILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPD
            HYTLRKISSLANSFLTIKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVK
            ALGELDILLQWMEETE"

ORIGIN
Alignment Scores:
Pred. No.:
Score:                      3.22e-72        Length:         926
Percent Similarity:         753.00          Matches:        144
Best Local Similarity:      100.00%         Conservative:   0
Query Match:                100.00%         Mismatches:     0
DB:                         6               Indels:         0
                                            Gaps:           0

US-10-789-251-26 (1-144) x CS110179 (1-926)

Qy    1  CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer  20
Db  141  TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGGCAGT  200

Qy   21  ValGlnAlaLysAspGlyAsnIleAspIleArgLeuIleLeuArgArgThrGluSerLeuGln  40
Db  201  GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA  260

Qy   41  AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp  60
Db  261  GACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGAC  320

Qy   61  ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu  80
Db  321  AGGGTATTTAAAAACTACCAGACACCCCTGACCATTATACTCTCCCGGAAGATCAGCAGCCTC  380

Qy   81  AlaAsnSerPheLeuThrIleLysAspLeuArgLeuCysHisAlaHisMetThrCys  100
Db  381  GCCAATTCCTTTACCATCAAGGAGGACCTTCGGCTCTGTCATGCCCACATGACATGC  440

Qy  101  HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu  120
Db  441  CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  500

Qy  121  GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet  140
Db  501  GAACCTCAGCCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG  560

Qy  141  GluGluThrGlu  144
Db  561  GAGGAGACAGAA  572
```

(Left column, lower)

```
RESULT 4
LOCUS         CS110179         926 bp    DNA    linear    PAT 22-JUN-2005
DEFINITION    Sequence 1 from Patent WO2005052000.
ACCESSION     CS110179
VERSION       CS110179.1    GI:68148437
KEYWORDS
SOURCE        Homo sapiens (human)
  ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
REFERENCE     1
```

(Right column, lower)

```
RESULT 5
LOCUS         AR342856         926 bp    DNA    linear    PAT 17-AUG-2003
DEFINITION    Sequence 1 from patent US 6576743.
ACCESSION     AR342856
VERSION       AR342856.1    GI:33738131
KEYWORDS
SOURCE        Unknown.
```

ORGANISM Unknown.
          Unclassified.
REFERENCE   1 (bases 1 to 926)
  AUTHORS   Conklin,D.C. and Haldeman,B.A.
  TITLE   Mammalian cytokine-like polypeptide-10
  JOURNAL   Patent: US 6576743-A 1 10-JUN-2003;
            ZymoGenetics, Inc.; Seattle, WA
FEATURES   Location/Qualifiers
     source   1..926
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

US-10-789-251-26 (1-144) x AR342856 (1-926)

Alignment Scores:
Pred. No.:
Score: 3.22e-72
                       753.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 6
DB:

Length: 926
Matches: 144
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

```
Qy    1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGCAGT 200

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261 GACACAAAGCCTGCGAATCGATGCTGCCTCCTGCTGAGACATCTTATCTGGAC 320

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440

Qy  101 HisGlyGluGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  441 CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

Qy  121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  501 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATCTTGCTGCAATGGATG 560

Qy  141 GluGluThrGlu 144
         ||||||||||||
Db  561 GAGGAGACAGAA 572
```

RESULT 6
LOCUS   AF224266   926 bp   mRNA   linear   PRI 24-JAN-2001
DEFINITION Homo sapiens four alpha helix cytokine (ZCYTO10) mRNA, ZCYTO10-1
            allele, complete cds.
ACCESSION   AF224266
VERSION   AF224266.1 GI:7109206
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 926)
  AUTHORS   Blumberg,H., Conklin,D., Xu,W.F., Grossmann,A., Brender,T.,
            Carollo,S., Eagan,M., Foster,D., Haldeman,B.A., Hammond,A.,
            Haugen,H., Jelinek,L., Kelly,J.D., Madden,K., Maurer,M.F.,
            Parrish-Novak,J., Prunkard,D., Sexson,S., Sprecher,C., Waggie,K.,
            West,J., Whitmore,T.E., Yao,L., Kuechle,M.K., Dale,B.A. and
            Chandrasekher,Y.A.
  TITLE   Interleukin 20: discovery, receptor identification, and role in
            epidermal function
  JOURNAL   Cell 104 (1), 9-19 (2001)
   PUBMED   11163236
REFERENCE   2 (bases 1 to 926)
  AUTHORS   Conklin,D., Grossmann,A., Haldeman,B. and O'Hara,P.
  TITLE   Homo sapiens four alpha helix cytokine allele 1
  JOURNAL   Unpublished
REFERENCE   3 (bases 1 to 926)
  AUTHORS   Conklin,D., Grossmann,A., Haldeman,B. and O'Hara,P.
  TITLE   Direct Submission
  JOURNAL   Submitted (12-JAN-2000) Biomolecular Informatics, ZymoGenetics,
            Inc., 1201 Eastlake Ave. East, Seattle, Wa. 98102, USA
FEATURES   Location/Qualifiers
     source   1..926
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /map="1q32.2"
     gene   1..926
                     /gene="ZCYTO10"
                     /allele="1"
     CDS   45..575
                     /gene="ZCYTO10"
                     /allele="1"
                     /codon_start=1
                     /product="four alpha helix cytokine"
                     /protein_id="AAF36679.1"
                     /db_xref="GI:7109207"
                     /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRN
                     GFSDIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPD
                     HYTLRKISSLANSPLTIKKDLRLCHAHWTCHGEEAMKKYSQILSHFEKLEPQAAVVK
                     ALGELDILLQWMEETE"
ORIGIN

US-10-789-251-26 (1-144) x AF224266 (1-926)

Alignment Scores:
Pred. No.:
Score: 3.22e-72
                       753.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 8
DB:

Length: 926
Matches: 144
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

```
Qy    1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGCAGT 200

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261 GACACAAAGCCTGCGAATCGATGCTGCCTCCTGCTGAGACATCTTATCTGGAC 320

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440

Qy  101 HisGlyGluGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  441 CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

Qy  121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  501
```

```
Db      501 GAACCTCAGGCAGCAGTTGTGTGAGGCTTTGGGGGAACTAGACATTCTTCGCAATGGATG 560

Qy      141 GluGluThrGlu 144

Db      561 GAGGAGACAGAA 572
```

```
RESULT 7

CS123418
LOCUS       CS123418           462 bp   DNA      linear  PAT 16-JUL-2005
DEFINITION  Sequence 18 from Patent WO2005058946.
ACCESSION   CS123418
VERSION     CS123418.1  GI:70911957
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 462)
  AUTHORS   Chan,C.
  TITLE     Methods for enhancing expression of recombinant proteins
  JOURNAL   Patent: WO 2005058946-A 18 30-JUN-2005;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..462
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
```

```
US-10-789-251-26 (1-144) x CS123418 (1-462)

Alignment Scores:

Pred. No.:                    4.06e-72
Score:                        749.00          Length:        462
Percent Similarity:           100.00%         Matches:       143
Percent Identity:             100.00%         Conservative:    0
Best Local Similarity:        99.31%          Mismatches:      1
Query Match:                  99.47%          Indels:          0
DB:                           6               Gaps:            0
```

```
Qy      1 CysValIleAlaThrAsnLeuGlnGlnIleArgAsnGlyPheSerAspIleArgGlySer 20
          |||||||||||||||||||||||||||||||||||::|||||||||||||||||||||||
Db      1 TGTGTGATCGCCACAAACCTGCAGGAAATCCGTAACGGTTCTTCTGAGATCCGTGGCAGC 87

Qy     21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     88 GTGCAGGCCAAAGATGGTAACATTGACATCCGTATCCTGCGTCGTACCGAGTCTCTGCAG 147

Qy     41 AspThrLysProAlaAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 GACACCAAAACCGGCGAACCGTTGCTCCTGCGGCGCCACCTGCTCTGTATCTGGAC 207

Qy     61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    208 CGTGTTTTCAAAAACTACCAGACCCCGGACCACTATACCCTGCGTAAAATCAGCAGCCTG 267

Qy     81 AlaAsnSerPheLeuThrIleLeuLysGlyLysAspLeuArgLeuCysHisIleAlaHisMetThrCys 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    268 GCCAACTCCTTCCTGACCATCAAAGAACCTGCGTCTGTCTGCCACCATGACCTGC 327

Qy    101 HisCysGlyCysGluGluValMetLysGlyTyrSerGlnIleLeuSerHisPheGlyLysLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    328 CACTGTGGTGAGGAGGCCAATGAAAAAATACAGCCACTTCGAAAAACTG 387

Qy    121 GluProGlnAlaAlaAsnArgValValIleLysGlyAlaLeuGlyTyrGluLeuAspIleLeuGlnIleTrpMet 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    388 GAACCGCAGGCAGCAGTGGTGAAAGCTCTCGGGTATGAACTGGACATTCTGCTGCAGTGGATG 447

Qy    141 GluGluThrGlu 144
          ||||||||||||
Db    448 GAGGAGACCGAA 459
```

```
Db
BC069311
LOCUS       BC069311           531 bp   mRNA     linear  PRI 06-JUL-2005
DEFINITION  Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96907
            IMAGE:7262116), complete cds.
ACCESSION   BC069311
VERSION     BC069311.1  GI:47480994
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 531)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 531)
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (29-APR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Baylor Human Genome Sequencing Center
            cDNA Library Preparation: Baylor Human Genome Sequencing Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: Amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRBR Plate: 1 Row: c Column: 2.
FEATURES             Location/Qualifiers
     source          1..531
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:96907 IMAGE:7262116"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_244"
                     /note="Vector: pPCR-Script Amp SK(+)"
     gene            1..531
                     /gene="IL20"
                     /note="synonyms: ZCYTO10, IL10D, IL-20, MGC96907"
                     /db_xref="GeneID:50604"
```

```
RESULT 8
```

RESULT 9

US-10-789-251-26 (1-144) x BC069311 (1-531)

```
Qy          1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
              TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGGAGATACGGGGCAGT 156
Db         97 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGGAGATACGGGGCAGT 156
```

ORIGIN

CDS
    /db_xref="MIM:605619"
    1..531
    /gene="IL20"
    /codon_start=1
    /product="interleukin 20, precursor"
    /protein_id="AAH69311.1"
    /db_xref="GI:47480995"
    /db_xref="GeneID:50604"
    /db_xref="MIM:605619"
    /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTINLGSCVIATNLQEIRN
    GFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPD
    HYTLRKISSLANSFLTIKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVK
    ALGEIDILLQWMEETE"

ORIGIN

Alignment Scores:
Pred. No. :   1..531
Score: 749.00
Percent Similarity: 100.00%
Best Local Similarity: 99.31%
Query Match: 99.47%
DB: 8

              Length: 531
              Matches: 143
              Conservative: 1
              Mismatches: 0
              Indels: 0
              Gaps: 0

```
Qy         21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
              GTGCAAGCCAAAGATGGAAACATTGACATCAGAAATCTTAAGGAGAGGACTGAGTCTTTGCAA 216
Db        157 GTGCAAGCCAAAGATGGAAACATTGACATCAGAAATCTTAAGGAGAGGACTGAGTCTTTGCAA 216

Qy         41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
              GACACAAAGCCTGCGAATCGATGCTGCCTCCTCCGCCATTTGCTAAGACTCTATCTGGAC 276
Db        217 GACACAAAGCCTGCGAATCGATGCTGCCTCCTCCGCCATTTGCTAAGACTCTATCTGGAC 276

Qy         61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
              AGGGTATTTAAAAACTACCAGACACCCGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336
Db        277 AGGGTATTTAAAAACTACCAGACACCCGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336

Qy         81 AlaAsnSerPheLeuThrIleLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
              GCCAATTCCTTTCTTACCATCAAGGAGGACCTTCGGCTCTGTCATCCCCACATGACATGC 396
Db        337 GCCAATTCCTTTCTTACCATCAAGGAGGACCTTCGGCTCTGTCATCCCCACATGACATGC 396

Qy        101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
              CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 456
Db        397 CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 456

Qy        121 GluProGlnAlaAlaValValLysAlaLeuGlyGluIleAspIleLeuLeuGlnTrpMet 140
              GAACCTCAGGCAGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 516
Db        457 GAACCTCAGGCAGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 516

Qy        141 GluGluThrGlu 144
              GAGGAGACAGAA 528
Db        517 GAGGAGACAGAA 528
```

LOCUS   BC069364   531 bp   mRNA   linear   PRI 30-JUN-2004
DEFINITION Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96919
            IMAGE:7262128), complete cds.
ACCESSION   BC069364
VERSION   BC069364.1   GI:47479475
KEYWORDS   MGC.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 531)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

REFERENCE   2 (bases 1 to 531)
  AUTHORS   Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE   Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   1 (bases 1 to 531)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (29-APR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Baylor Human Genome Sequencing Center
            cDNA Library Preparation: Baylor Human Genome Sequencing Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRBR Plate: 1 Row: d Column: 2.

FEATURES   Location/Qualifiers
     source   1..531
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:96919 IMAGE:9606"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_244"
                     /note="Vector: pPCR-Script Amp SK(+)"
     gene   1..531
                     /gene="IL20"
                     /note="synonyms: ZCYTO10, IL10D, IL-20"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
     CDS   1..531
                     /gene="IL20"
                     /codon_start=1
                     /product="interleukin 20, precursor"
                     /protein_id="AAH69364.1"
                     /db_xref="GI:47479476"
                     /db_xref="taxon:9606"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
                     /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTINLGSCVIATNLQEIRN
                     GFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPD
                     HYTLRKISSLANSFLTIKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVK
                     ALGEIDILLQWMEETE"
ORIGIN

```
Alignment Scores:
Pred. No.:
Score:                  4.73e-72        Length:          531
Percent Similarity:     749.00          Matches:         143
Best Local Similarity:  100.00%         Conservative:    1
Query Match:            99.31%          Mismatches:      0
DB:                     99.47%          Indels:          0
                        8               Gaps:            0

US-10-789-251-26 (1-144) x BC069364 (1-531)

Qy    1 CysValIleAlaThrAsnLeuGlnGlyIleArgAsnGlyPheSerAspIleArgGlySer  20
Db   97 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGCGCAGT  156

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgAspThrGluSerLeuGln   40
Db  157 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGGACACTGAGTCTTTGCAA  216

Qy   41 AspThrLysProAlaAsnArgCysGlyLeuLeuArgHisLeuArgGluTyrLeuAsp     60
Db  217 GACACAAAGCCTGCGAATCGATGCGGTCTCCTCCTGCCCATTGACCTAAGACTCTATCTGGAC  276

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleLeuSerLeu   80
Db  277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGAAAGATCAGCAGCCTC  336

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys  100
Db  337 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTGTCACGCCCACATGACATGC  396

Qy  101 HisCysGlyGlyCysHisGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu  120
Db  397 CATTGTGGGGGATGAGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  456

Qy  121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet  140
Db  457 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG  516

Qy  141 GluGluThrGlu  144
Db  517 GAGGAGACAGAA  528
```

```
RESULT 10
BC069398
LOCUS       BC069398                531 bp    mRNA    linear    PRI 18-JUL-2005
DEFINITION  Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96931
            IMAGE:7262140), complete cds.
ACCESSION   BC069398
VERSION     BC069398.1  GI:47481040
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homindiidae; Homo.
REFERENCE   1  (bases 1 to 531)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   NIH MGC Project
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 531)
  AUTHORS   NIH MGC Project
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (29-APR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Betheda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Baylor Human Genome Sequencing Center
            cDNA Library Preparation: Baylor Human Genome Sequencing Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRBR Plate: 1 Row: e Column: 2.
FEATURES             Location/Qualifiers
     source          1..531
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:96931 IMAGE:7262140"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_244"
                     /note="Vector: pPCR-Script Amp SK(+)"
     gene            1..531
                     /gene="IL20"
                     /note="synonyms: ZCYTO10, IL10D, IL-20, MGC96907"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
     CDS             1..531
                     /gene="IL20"
                     /codon_start=1
                     /product="interleukin 20, precursor"
                     /protein_id="AAH63398.1"
                     /db_xref="GI:47481041"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
                     /translation="MKASSLAFSLLLSAAFVLLWTPSTGLKTLNLGSCVIATNLQEIRN
                     GFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLRLYLDRVFKNYQTPD
                     HYTLRKISSLANSPLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVK
                     ALGELDILLQWMEETE"
ORIGIN

US-10-789-251-26 (1-144) x BC069398 (1-531)

Alignment Scores:
Pred. No.:
Score:                  4.73e-72        Length:          531
Percent Similarity:     749.00          Matches:         143
Best Local Similarity:  100.00%         Conservative:    1
Query Match:            99.31%          Mismatches:      0
DB:                     99.47%          Indels:          0
                        8               Gaps:            0

Qy    1 CysValIleAlaThrAsnLeuGlnGlyIleArgAsnGlyPheSerAspIleArgGlySer  20
Db   97 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGCGCAGT  156

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgAspThrGluSerLeuGln   40
```

```
db    157 GTGCAAGCCAAAGATGGAAAACAATTGACAATCAGAATCTTAAGGAGGACTGAGTCTTTGAA 216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 GACACAAAGCCTGCCAATCGATGCTGCCTCCTCGGCCAATTGCTAAGACTCTATCTGGAC 276
Qy     61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336
Qy     81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    337 GCCAATTCCTTCTTTACCATCAAGAAAGAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 396
Qy    101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    397 CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 456
Qy    121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    457 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 516
Qy    141 GluGlyThrGlu 144
          ||||||||||||
Db    517 GAGGAGACAGAA 528
```

RESULT 11
LOCUS   BC069425
DEFINITION Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96943
            IMAGE:7262152), complete cds.
ACCESSION   BC069425
VERSION   BC069425.1 GI:47479503
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 531)
  AUTHORS   Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
            Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
            B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
            Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
            GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
            Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
            Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
            SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
            Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
            Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,
            Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M,
            Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
            Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
            Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
            Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.
  TITLE   Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2 (bases 1 to 531)
  AUTHORS   Director MGC Project.
  TITLE   Direct Submission
  JOURNAL   Submitted (29-APR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
  CONSRTM   MGC Project
  COMMENT   Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Baylor Human Genome Sequencing Center
            cDNA Library Preparation: Baylor Human Genome Sequencing Center

FEATURES   Location/Qualifiers
     source   1..531
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:96943 IMAGE:7262152"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_244"
                     /note="Vector: pPCR-Script Amp SK(+)"
     gene   1..531
                     /gene="IL20"
                     /note="synonyms: ZCYTO10, IL10D, IL-20, MGC96907"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
     CDS   1..531
                     /gene="IL20"
                     /codon_start=1
                     /product="interleukin 20, precursor"
                     /protein_id="AAH69425.1"
                     /db_xref="GI:47479504"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
                     /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRN
                     GFSEIRGSSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPD
                     HYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVK
                     ALGELDILLQWMETE"

ORIGIN

US-10-789-251-26 (1-144) x BC069425 (1-531)

Alignment Scores:
  Pred. No.:
  Score: 4.73e-72
                           749.00   Length: 531
  Percent Similarity: 100.00%   Matches: 143
  Best Local Similarity: 99.31%   Conservative: 1
  Query Match: 99.47%   Mismatches: 0
                           8   Indels: 0
                                                        Gaps: 0

```
Qy      1 CysValIleLeuThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TGTGTGATCCGCCACAAAACCTTCAGGAAATACGAAAATGGAGATTTCTGAGATACGGAGT 156
Qy     21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        ...
Qy     41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 GACACAAAGCCTGCCAATCGATGCTGCCTCCTCGGCCAATTGCTAAGACTCTATCTGGAC 276
Qy     61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336
Qy     81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    337 GCCAATTCCTTCTTTACCATCAAGAAAGAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 396
Qy    101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    397 CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 456
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy    121 GluProGlnAlaAlaValValLysAlaLeuGlyLeuAspIleLeuLeuGlnTrpMet 140
Db    457 GAACCTCAGCGACAGCAGTTGTGAAGGCTTTGGGGGGAACTAGAACATTCTTCTGCAATGGATG 516

Qy    141 GluGluThrGlu 144
           ||||||||||||
Db    517 GAGGAGACAGAA 528
```

RESULT 12
BC069449

LOCUS   BC069449   531 bp   mRNA   linear   PRI 08-MAR-2005
DEFINITION Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96955
            IMAGE:7262164), complete cds.
ACCESSION   BC069449
VERSION   BC069449.1 GI:47480911
KEYWORDS   MGC.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 531)
  AUTHORS   Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
            Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
            B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
            Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
            GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
            Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
            Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
            SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
            Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
            Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,
            Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M,
            Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
            Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
            Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
            Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.
  TITLE   Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2 (bases 1 to 531)
  AUTHORS   Direct Submission
  TITLE   Direct Submission
  JOURNAL   Submitted (29-APR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
   REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Baylor Human Genome Sequencing Center
            cDNA Library Preparation: Baylor Human Genome Sequencing Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRBR Plate: 1 Row: g Column: 2.
FEATURES   Location/Qualifiers
     source   1..531
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:96955 IMAGE:7262164"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_244"
                     /note="Vector: pPCR-Script Amp SK(+)"
     gene   1..531
                     /gene="IL20"
                     /note="synonyms: ZCYTO10, IL10D, IL-20, MGC96907"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
     CDS   1..531
                     /gene="IL20"
                     /codon_start=1
                     /product="interleukin 20, precursor"
                     /protein_id="AAH69449.1"
                     /db_xref="GI:47480912"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
                     /translation="MKASSLAFSLLSAAPYLLWTPSTGLKTLNLGSSCVIATNLQEIRN
                     GFSSIRGSVQAKDGNIDIRILRRTESLQDTKPAARCCLLRHLLRIYLDRVFKNYQTPD
                     HYTLRKISSLANSFLTIKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVK
                     ALGELDILLQWMEETE"
ORIGIN

US-10-789-251-26 (1-144) x BC069449 (1-531)

Alignment Scores:
Pred. No.:   4.73e-72   Length: 531
Score: 749.00   Matches: 143
Percent Similarity: 100.00%   Conservative: 1
Best Local Similarity: 99.31%   Mismatches: 0
Query Match: 99.47%   Indels: 0
DB: 8   Gaps: 0
```

```
Qy     1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAsnIleArgGlySer 20
          ||||||||||||||||||||||||||||||||||||||||||| ::|||||||||||||||
Db    97 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTAACATAAGGGGCAGT 156

Qy    21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   157 GTGCAAGCCAAAGATGGAAACATTGACATCAGAAATCTTAGGAGGACTGAGTCTTTGCAA 216

Qy    41 AspThrLysProAlaAlaArgCysCysLeuLeuArgHisLeuLeuArgIleTyrLeuAsp 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   217 GACACAAAAGCCTGCGAATCGATGCTCCTCCTCCTGCGCCATTTGCTAAGACTCTATCGGAC 276

Qy    61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336

Qy    81 AlaAsnSerPheLeuThrIleLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   337 GCCAATTCCTTTCTTACCATCAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 396

Qy   101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   397 CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 456

Qy   121 GluProGlnAlaAlaValValLysAlaLeuGlyLeuAspIleLeuLeuGlnTrpMet 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   457 GAACCTCAGCGACAGCAGTTGTGAAGGCTTTGGGGGGAACTAGAACATTCTTCTGCAATGGATG 516

Qy   141 GluGluThrGlu 144
          ||||||||||||
Db   517 GAGGAGACAGAA 528
```

RESULT 13
BC069487

LOCUS   BC069487   531 bp   mRNA   linear   PRI 08-MAR-2005
DEFINITION Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96967
            IMAGE:7262176), complete cds.
ACCESSION   BC069487
VERSION   BC069487.1 GI:47480770

KEYWORDS   MGC.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1 (bases 1 to 531)
  AUTHORS   Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
             Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
             B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
             Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
             GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
             Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
             Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
             SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
             Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
             Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,
             Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M,
             Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
             Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
             Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
             Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE   Generation and initial analysis of more than 15,000 full-length
             human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2 (bases 1 to 531)
  AUTHORS   Director MGC Project.
  TITLE   Direct Submission
  JOURNAL   Submitted (29-APR-2004) National Institutes of Health, Mammalian
             Gene Collection (MGC), Cancer Genomics Office, National Cancer
             Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
             USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Baylor Human Genome Sequencing Center
             cDNA Library Preparation: Baylor Human Genome Sequencing Center
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Baylor College of Medicine Human Genome
             Sequencing Center
             Center code: BCM-HGSC
             Web site: http://www.hgsc.bcm.tmc.edu/cdna/
             Contact: amg@bcm.tmc.edu
             Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
             Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
             A.N., Gibbs, R.A.
             Clone distribution: MGC clone distribution information can be found
             through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             Series: IRBR Plate: 1 Row: h Column: 2.
FEATURES   Location/Qualifiers
     source   1..531
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:96967 IMAGE:7262176"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_244"
                     /note="Vector: pCR-Script Amp SK(+)"
     gene   1..531
                     /gene="IL20"
                     /note="synonyms: ZCYTO10, IL10D, IL-20, MGC96907"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605519"
     CDS   1..531
                     /gene="IL20"
                     /codon_start=1
                     /product="interleukin 20, precursor"
                     /protein_id="AAH69487.1"
                     /db_xref="GI:47480771"
                     /db_xref="GeneID:50604"

ORIGIN
                     /db_xref="MIM:605519"
                     /translation="MKASSLAPSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRN
                     GFSEIRGSVQAKDGNIDIRILRRTESLQDTRARNTGHCLLRHLLRYLYLDRVFKNYQTPD
                     HYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVK
                     ALGELDILLQWMEETE"

US-10-789-251-26 (1-144) x BC069487 (1-531)

Alignment Scores:
Pred. No.:
Score: 749.00
Percent Similarity: 100.00%
Best Local Similarity: 99.31%
Query Match: 99.47%
DB: 8

Length: 531
Matches: 143
Conservative: 1
Mismatches: 0
Indels: 0
Gaps: 0

Qy   1   CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer   20
             |||||||||||||||||||||||||||||||||||||||||||||||:::||||||||||
Db   1   TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGT   97

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln   40
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   157 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA   216

Qy   41 AspThrArgProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp   60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   217 GACACAAGACCTGCAAATCGATGCTGCCTCCTCCGGCATCTTAAGACTCTATCTGGAC   276

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu   80
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC   336

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys   100
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   337 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGCCTCTGTCATGCCCACATGACATGC   396

Qy   101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu   120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   397 CATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG   456

Qy   121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet   140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   457 GAACCTCAGGCAGCAGTTGTGAAAGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG   516

Qy   141 GluGluThrGlu   144
             ||||||||||||
Db   517 GAGGAGACAGA   528

RESULT 14
BC069523
BC069523
LOCUS   BC069523   531 bp   mRNA   linear   PRI 08-MAR-2005
DEFINITION Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96884
            IMAGE:7262093), complete cds.
ACCESSION   BC069523
VERSION   BC069523.1 GI:47479431
KEYWORDS   MGC.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 531)
  AUTHORS   Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
            Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
            B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
            Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
            GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
            Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
            Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
            SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
            Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
            Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,

Left column

```
REFERENCE   Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M,
            Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
            Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
            Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
            Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2 (bases 1 to 531)
  AUTHORS   Direct Submission
  TITLE     Direct Submission
  JOURNAL   Submitted (29-APR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
  COMMENT   Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Baylor Human Genome Sequencing Center
            cDNA Library Preparation: Baylor Human Genome Sequencing Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRBR Plate: 1 Row: a Column: 3.
FEATURES             Location/Qualifiers
     source          1..531
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:96884 IMAGE:7262093"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC 244"
                     /note="Vector: pCR-Script Amp SK(+)"
     gene            1..531
                     /gene="IL20"
                     /note="synonyms: ZCYTO10, IL10D, IL-20, MGC96907"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
     CDS             1..531
                     /gene="IL20"
                     /codon_start=1
                     /product="interleukin 20, precursor"
                     /protein_id="AAH69523.1"
                     /db_xref="GI:47479432"
                     /db_xref="GeneID:50604"
                     /db_xref="MIM:605619"
                     /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRN
                     GFSEIRGSVQAAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPD
                     HYTLRKISSLANSPLTIKKDLRLCHAHMTCHGEEAMKKYSQILSHFEKLEPQAAVVK
                     ALGELDILLQWMEETE"
ORIGIN
Alignment Scores:
  Pred. No.:
  Score:                4.73e-72
  Percent Similarity:   749.00
  Best Local Similarity:100.00%
  Query Match:          99.31%
  DB:                   99.47%

US-10-789-251-26 (1-144) x BC069523 (1-531)

                                    Length:        531
                                    Matches:       143
                                    Conservative:  1
                                    Mismatches:    0
                                    Indels:        0
                                    Gaps:          0
```

Right column

```
Qy    1 CysValIleLeuAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
        |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db   97 TGTGTGATCGGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGGATATACGGGGCAGT 156

Qy   21 ValGlnAlaAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  157 GTGCAAGCCAAAGATGGAAACATTGACATTCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 216

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  217 GACACAAAGCCTGCGAACAGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGAC 276

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  277 AGGGTATTTAAAAACTACCAGACCCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 336

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  337 GCCAATTCCTTTCTTACCATCAAGAAAGACCTCCGGCTTTGTCATGCCCACATGACATGC 396

Qy  101 HisGlyCysGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  397 CATTGTGGGGGAGGAAGCCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 456

Qy  121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  457 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 516

Qy  141 GluGluThrGlu 144
        ||||||||||||
Db  517 GAGGAGACAGAA 528
```

```
RESULT 15
LOCUS       BC069559                 531 bp    mRNA    linear   PRI 08-MAR-2005
DEFINITION  Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96896
            IMAGE:7262105), complete cds.
ACCESSION   BC069559
VERSION     BC069559.1  GI:47480991
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 531)
  AUTHORS   Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
            Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
            B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
            Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
            GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
            Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
            Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
            SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
            Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
            Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,
            Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M,
            Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
            Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
            Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
            Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2 (bases 1 to 531)
  AUTHORS   Direct Submission
  TITLE     Direct Submission
  JOURNAL   Submitted (29-APR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
```

REMARK
COMMENT   NIH-MGC Project URL: http://mgc.nci.nih.gov
           Contact: MGC help desk
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Baylor Human Genome Sequencing Center
           cDNA Library Preparation: Baylor Human Genome Sequencing Center
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Baylor College of Medicine Human Genome
           Sequencing Center
           Center code: BCM-HGSC
           Web site: http://www.hgsc.bcm.tmc.edu/cdna/
           Contact: ang@bcm.tmc.edu
           Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
           Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
           A.N., Gibbs, R.A.

           Clone distribution: MGC clone distribution information can be found
           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
           Series: IRBR Plate: 1 Row: b Column: 3.

FEATURES   Location/Qualifiers
     source   1..531
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="MGC:96896 IMAGE:7262105"
               /tissue_type="PCR rescued clones"
               /clone_lib="NIH_MGC_244"
               /note="Vector: pCR-Script Amp SK(+)"
     gene   1..531
               /gene="IL20"
               /note="synonyms: ZCYTO10, IL10D, IL-20, MGC96907"
               /db_xref="GeneID:50604"
               /db_xref="MIM:605619"
     CDS   1..531
               /gene="IL20"
               /codon_start=1
               /product="interleukin 20, precursor"
               /protein_id="AAH69559.1"
               /db_xref="GI:47480992"
               /db_xref="GeneID:50604"
               /db_xref="MIM:605619"
               /translation="MKASSLAFSLLSAAFYLLWTPSTGLKTNLGSCVIATNLQEIRN
               GFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPD
               HYTLRKISSLANSFLTIKKDLRLCHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVK
               ALGELDILLQWMEETE"

ORIGIN

Alignment Scores:
Pred. No.:   4.73e-72
Score: 749.00   Length: 531
Percent Similarity: 100.00%   Matches: 143
Best Local Similarity: 99.31%   Conservative: 1
Query Match: 99.47%   Mismatches: 1
DB: 8   Indels: 0
                                     Gaps: 0

US-10-789-251-26 (1-144) x BC069559 (1-531)

```
Qy    1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer   20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   97 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGCGGCAGT  156

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln   40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  157 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA  216

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  217 GACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGAC  276

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu   80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC  336

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys  100
```

                                                                  Search completed: December 28, 2005, 12:45:48
                                                                  Job time : 2950 secs

```
Db  337 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTTGTCATGCCCACATGACTGC  396

Qy  101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu  120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db  397 CATTGTGGCGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  456

Qy  121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet  140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  457 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG  516

Qy  141 GluGluThrGlu  144
        ||||||||||||
Db  517 GAGGAGACAGAA  528
```

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: December 28, 2005, 11:43:12 ; Search time 499 Seconds
                                                         (without alignments)
                                                         1923.278 Million cell updates/sec

Title: US-10-789-251-26
Perfect Score: 753
Sequence: 1 CVIATNLQEIRNGFSDIRGS.........AVVKALGBELDILLQWMEETE 144

Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop   6.0 , Fgapext 7.0
                Delop   6.0 , Delext   7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
 -MODEL=frame+_p2n.model -DEV=xlp
 -Q=/cgn2_1/USPTO_spool_p/US10789251/runat_23122005_152435_19737/app_query.fasta_1.327
 -DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
 -USER=US10789251 @CGN_1_1_1096 @runat_23122005_152435_19737 -NCPU=6 -ICPU=3
 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   N_Geneseq_21:*
          1:     geneseqn1980s:*
          2:     geneseqn1990s:*
          3:     geneseqn2000s:*
          4:     geneseqn2001as:*
          5:     geneseqn2001bs:*
          6:     geneseqn2002as:*
          7:     geneseqn2002bs:*
          8:     geneseqn2003as:*
          9:     geneseqn2003bs:*
         10:     geneseqn2003cs:*
         11:     geneseqn2003ds:*
         12:     geneseqn2004as:*
         13:     geneseqn2004bs:*
         14:     geneseqn2005s:*

                                    SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	753	100.0	528	12	ADM95042	Adm95042 Human Int
2	753	100.0	531	14	ADV42800	Adv42800 Human psy
3	753	100.0	926	2	AAX77692	Aax77692 Human Zcy
4	753	100.0	926	9	ACF05161	Acf05161 Polynucle

5	753	100.0	926	10	AAD61821	Human cyt
6	753	100.0	926	10	ADG46668	Human cyt
7	753	100.0	926	12	ADQ88066	Human Zcy
8	753	100.0	926	13	ADR16327	Human cyt
9	753	100.0	926	13	ADR24325	Breast ca
10	753	100.0	926	13	ADS18362	Human Zcy
11	753	100.0	926	14	AEA50048	Full leng
12	749	99.5	462	8	AEA28786	Human int
13	749	99.5	462	8	ABV75151	Human int
14	749	99.5	462	8	AEB26649	EC sequen
15	749	99.5	513	8	ABV75154	Human int
16	749	99.5	528	12	ADL15289	Human LP8
17	749	99.5	867	6	ABQ74562	Human LP8
18	749	99.5	867	6	ABV73092	Human CDN
19	749	99.5	925	12	ADN12153	Interleuk
20	746	99.1	926	12	ADS31716	DNA encod
21	746	99.1	926	13	ADS92718	DNA encod
22	739	99.1	1571	3	AAA37138	Human PRO
23	739	98.1	1571	4	AAF54484	Primer #1
24	739	98.1	1571	4	AAS21292	Human CDN
25	739	98.1	1571	4	AAS21516	Human CDN
26	739	98.1	1571	4	AAS46229	Human DNA
27	739	98.1	1571	4	AAF92126	Human PRO
28	739	98.1	1571	6	ABK33644	CDNA enco
29	739	98.1	1571	6	ABS74446	Human CDN
30	739	98.1	1571	6	ABL88214	Human PRO
31	739	98.1	1571	6	ABL95703	Human ang
32	739	98.1	1571	7	ADY31957	Novel hum
33	739	98.1	1571	8	ACA89679	CDNA enco
34	739	98.1	1571	8	ACA73689	CDNA enco
35	739	98.1	1571	8	ACA06004	Human sec
36	739	98.1	1571	8	ACA66838	CDNA enco
37	739	98.1	1571	8	ACA91232	Novel hum
38	739	98.1	1571	8	ACD81609	Human CDN
39	739	98.1	1571	8	ACF20413	Human PRO
40	739	98.1	1571	8	ACF19799	Human sec
41	739	98.1	1571	8	ACD22087	Human sec
42	739	98.1	1571	8	ACF13252	Human sec
43	739	98.1	1571	8	ACD25355	Human sec
44	739	98.1	1571	8	ACF00404	Human sec
45	739	98.1	1571	8	ACA60431	Novel hum

                                    ALIGNMENTS

RESULT 1
ADM95042

ID   ADM95042 standard; DNA; 528 BP.
XX
AC   ADM95042;
XX
DT   17-JUN-2004 (first entry)
XX
DE   Human Interleukin-20 (IL-20) gene SeqID4.
XX
KW   colon cancer; interleukin 20 receptor alpha chain;
KW   IL-20 receptor alpha chain; cytostatic; gene; ds; human.
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT
FT   CDS   1..528
FT   /*tag= a
FT   /product= "Human Interleukin-20 (IL-20) protein"
FT   /partial
FT   /note= "No stop codon"
XX
PN   JP2004075569-A.
XX
PD   11-MAR-2004.
XX
PF   12-AUG-2002; 2002JP-00234880.

```
PR   12-AUG-2002; 2002JP-00234880.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
DR   WPI; 2004-320878/30.
DR   P-PSDB; ADM95041.
XX
PT   Agent useful for prevention and/or treatment of colon cancer, comprises
PT   interleukin 20 (IL-20), IL-20 receptor alpha chain, IL-20 receptor beta
PT   chain.
XX
PS   Disclosure; SEQ ID NO 10; 50pp; Japanese.
XX
CC   This invention relates to a novel agent for prevention and/or treatment
CC   of colon cancer, comprising of the interleukin 20 (IL-20) receptor alpha
CC   chain, its partial peptide or salt. The invention may be useful for the
CC   development of compounds with a cytostatic activity. A diagnostic agent is
CC   useful for preventing and/or treating colon cancer. By using IL-20, its
CC   useful for diagnosis of colon cancer. By using IL-20, IL-20 receptor, its
CC   salt or its peptide, compounds that have altered binding property towards
CC   them can be efficiently screened. The present sequence is that of a gene
CC   which encodes the human Interleukin-20 protein and which is related to
CC   the invention.
XX
SQ   Sequence 528 BP; 148 A; 129 C; 122 G; 129 T; 0 U; 0 Other;

US-10-789-251-26 (1-144) x ADM95042 (1-528)

Alignment Scores:
Pred. No.:
Score:                    5.13e-87
                          753.00
Percent Similarity:       100.00%
Best Local Similarity:    100.00%
Query Match:              12

Length:         528
Matches:        144
Conservative:   0
Mismatches:     0
Indels:         0
Gaps:           0

Qy   1   CysValIleAlaThrAsnLeuGlnGlluLeuArgAsnGlyPheSerAspIleArgGlySer   20
Db   97  TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCGACATACGGGCGAGT   156

Qy   21  ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln   40
Db   157 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA   216

Qy   41  AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp   60
Db   217 GACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTTCTATCTGGAC   276

Qy   61  ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu   80
Db   277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC   336

Qy   81  AlaAsnSerPheLeuThrIleLysGlyAspLeuArgLeuCysHisAlaHisMetThrCys   100
Db   337 GCCAATTCCTTTCTTACCATCAAGGGAGACCTCCGGCTCTGTCATGCCCACATGACATGC   396

Qy   101 HisCysGlyCysGlluGluAlaMetLysGlyTyrSerGlnIleLeuSerHisPheGlyLysLeu   120
Db   397 CATTGTGGGGAGGAAGCAATGAAAGGAAATACAGCGCAGATTCTGAGTCACTTTGAAAAGCTG   456

Qy   121 GlnProGlnAlaLaAlaValValLysValGlyValGlyLeuAspIleLeuGlnTrpMet   140
Db   457 GAACCTCAGCGCAGCAGTTGTTGGGAGGGACTAGACATTCTTCTGCAATGGATG   516

Qy   141 GluGlyGluThrGlu   144
Db   517 GAGGAGACAGGA   528

RESULT 2
ADV42800
ID   ADV42800 standard; cDNA; 531 BP.
XX
AC   ADV42800;
```

```
XX
DT   10-MAR-2005 (first entry)
XX
DE   Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 428.
XX
KW   microarray; psychoneuroendocrinimmune; chronic fatigue;
KW   non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW   cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200410899-A2.
XX
PD   16-DEC-2004.
XX
PF   04-JUN-2004; 2004WO-US017686.
XX
PR   04-JUN-2003; 2003US-04759159P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Nicholson A, Vernon SD;
XX
DR   WPI; 2005-031682/03.
XX
PT   New microarray comprising probes for genes involved in
PT   psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT   condition associated with PNI activity, e.g., inflammatory or infectious
PT   diseases.
XX
PS   Claim 1; SEQ ID NO 428; 254pp; English.
XX
CC   The invention relates to a new microarray which comprises probes for
CC   genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC   microarray is useful in diagnosing a condition associated with PNI
CC   activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC   cancer and infection. The present sequence represents a
CC   psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC   specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC   SEQ ID NO 1829 are provided.
XX
SQ   Sequence 531 BP; 149 A; 129 C; 123 G; 130 T; 0 U; 0 Other;

US-10-789-251-26 (1-144) x ADV42800 (1-531)

Alignment Scores:
Pred. No.:
Score:                    5.18e-87
                          753.00
Percent Similarity:       100.00%
Best Local Similarity:    100.00%
Query Match:              14

Length:         531
Matches:        144
Conservative:   0
Mismatches:     0
Indels:         0
Gaps:           0

Qy   1   CysValIleAlaThrAsnLeuGlnGlluLeuArgAsnGlyPheSerAspIleArgGlySer   20
Db   97  TGTGTGATCGGCCACAAACCTTCAGGAAATACGGAAATGGATTTTCTGACACATACGGGGGCGAGT   156

Qy   21  ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln   40
Db   157 GTGCAAGCCAAAGATGGAAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA   216

Qy   41  AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp   60
Db   217 GACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTTCTTATCTGGAC   276

Qy   61  ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu   80
Db   277 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC   336

Qy   81  AlaAsnSerPheLeuThrIleLysGlyAspLeuArgLeuCysHisAlaHisMetThrCys   100
Db   337 GCCAATTCCTTTCTTACCATCAAGGGAGACCTCCGGCTCTGTCATGCCCACATGACATGC   396
```

```
Qy  101 HisCysGlyGluLeuAlaMetLeuLysTyrSerGlnIleIleLeuSerHisPheGluLysLeu 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  397 CATTGTGGGGAGGAAGCAATGAAGAAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 456
Qy  121 GluProGlnIleAlaAlaValValLysBAlaLeuGlyLeuLeuAspIleLeuLeuGlnTrpMet 140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  457 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 516
Qy  141 GluGluThrGlu 144
        ||||||||||||
Db  517 GAGGAGACAGAA 528
```

CC   be therapeutically useful in the regeneration of the gastrointestinal
CC   tract or oral cavity, as well as in the treatment of asthma, and other
CC   diseases of the tracheobronchial tract such as bronchitis. Zcyto10
CC   polypeptides may also be useful to promote wound healing, and to increase
CC   platelet count, e.g. in cancer patients who experience thrombocytopenia
CC   due to chemotherapy or radiation therapy
XX
SQ   Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

RESULT 3

AAX77692

ID   AAX77692 standard; cDNA; 926 BP.
XX
AC   AAX77692;
XX
DT   09-AUG-1999 (first entry)
XX
DE   Human Zcyto10 allele 1 cDNA.
XX
KW   Zcyto10; four alpha helix cytokine; vulnerary; cytostatic; growth factor; maintenance factor;
KW   anti-inflammatory; anti-asthmatic;
KW   trachea; salivary gland; stomach; pancreas; muscle; gene therapy; cancer;
KW   proliferation; differentiation; modulator; gastrointestinal tract;
KW   oral cavity; asthma; tracheobronchial tract; bronchitis; wound healing;
KW   platelet count; thrombocytopenia; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   45..575
FT   /*tag= a
FT   /product= "Zcyto10"
XX
PN   WO9927103-A1.
XX
PD   03-JUN-1999.
XX
PF   25-NOV-1998; 98WO-US025228.
XX
PR   26-NOV-1997; 97US-00979156.
XX
PA   (ZYMO) ZYMOGENETICS INC.
PI   Conklin DC, Haldeman BA, Grossmann A;
XX
DR   WPI: 1999-357840/30.
DR   P-PSDB; AAY08661.
XX
PT   New mammalian cytokine-like polynucleotide useful in the treatment of
PT   asthma and bronchitis.
XX
PS   Claim 3; Page 63-64; 82pp; English.
XX
CC   This invention describes a novel mammalian four alpha helix cytokine
CC   designated Zcyto10 which has vulnerary, cytostatic, anti-inflammatory,
CC   anti-asthmatic and haemostatic activity. Zcyto10 may be a growth factor and/or
CC   maintenance factor in the trachea and salivary glands, stomach, pancreas
CC   and muscle. Zcyto10 polynucleotides are useful as sources of primers and
CC   probes, and to determine if the Zcyto10 gene is present on chromosome 1,
CC   or to detect any mutations that may have occurred. Zcyto10
CC   polynucleotides are also useful as gene therapy reagents. The Zcyto10
CC   polypeptide, its fragments, and antibodies, as well as compounds
CC   identified as having binding affinity to Zcyto10, should be useful in the
CC   treatment of conditions associated with abnormal physiology or
CC   development, including abnormal proliferation, e.g. cancerous conditions,
CC   or degenerative conditions or altered immunity. The products are also
CC   useful for modulating cell proliferation, cell differentiation or
CC   cytokine production in the prevention or treatment of conditions
CC   characterized by abnormal cell proliferation, cell differentiation or
CC   cytokine production. Zcyto10 polypeptides, agonists and antagonists may

US-10-789-251-26 (1-144) x AAX77692 (1-926)

```
Alignment Scores:
Pred. No.:                            1.17e-86     Length:        926
Score:                753.00                       Matches:        144
Percent Similarity:   100.00%                      Conservative:     0
Best Local Similarity: 100.00%                     Mismatches:       0
Query Match:          100.00%                      Indels:           0
DB:                        2                       Gaps:             0
```

```
Qy    1 CysValIleAlaThrAsnLeuGlnGlnIleIleArgAsnGlyPheSerAspIleArgGlySer  20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141 TGTGTGATCGCCACAAACCTTCAGGAAATACGGAAATGGATTTTCTGACATACGGGGCAGT 200
Qy   21 ValGlnAlaLysAspAlaSerGlyAsnIleAspIleArgIleLeuArgAsnThrGluSerGln  40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201 GTGCAAGCCAAAGATGGAAACAATCATTGACATTAGAATTCTTAGGAGGACTGAGTCTTGCAA 260
Qy   41 AspThrLysProAlaAlaAsnArgCysLeuLeuLeuArgHisLeuLeuLeuArgLeuTyrLeuAsp  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261 GACACAAAAGCCTGCCGAATCGANTCGNTGCCTCCTGCGCGCCATTTGCTAAGACTCTATCTGGAC 320
Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu  80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  321 AGGGTATTTAAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380
Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  381 GCCAATTCCTTCTTTACCATCAAGAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440
Qy  101 HisCysGlyGluLeuAlaMetLeuLysTyrSerGlnIleIleLeuSerHisPheGluLysLeu 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  441 CATTGTGGGGAGGAAGCAATGAAGAAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500
Qy  121 GluProGlnIleAlaAlaValValLysBAlaLeuGlyLeuLeuAspIleLeuLeuGlnTrpMet 140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  501 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 560
Qy  141 GluGluThrGlu 144
        ||||||||||||
Db  561 GAGGAGACAGAA 572
```

RESULT 4

ACF05161

ID   ACF05161 standard; cDNA; 926 BP.
XX
AC   ACF05161;
XX
DT   06-NOV-2003 (first entry)
XX
DE   Polynucleotide encoding human interleukin-20.
XX
KW   Human; interleukin-20; IL-20; cervical cancer; cytostatic; virucide;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   45..575
FT   /*tag= a
FT   /product= "Human IL-20"
FT   sig_peptide   45..116
FT   /*tag= b
FT   mat_peptide   117..572

```
PT
XX
PN      WO200305I384-AI.
XX
PD      26-JUN-2003.
XX
PF      17-DEC-2002; 2002WO-US040309.
XX
PR      17-DEC-2001; 2001US-0341783P.
XX
PA
PA      (LUNN/) LUNN P G.
XX
PI      Chandrasekher YA, McKernan PA;
XX
DR      WPI; 2003-569114/53.
DR      P-PSDB; ABR62464.
XX
PT      Inhibiting the growth and/or proliferation of cervical cancer cells,
PT      useful for treating cervical cancer or human papilloma virus infection,
PT      comprises bringing Interleukin-20 (Il-20) into contact with the cervical
PT      cancer cells.
XX
PS      Disclosure; Page 11-12; 26pp; English.
XX
CC      The present sequence is that of a polynucleotide encoding human
CC      interleukin-20 (IL-20), including the signal sequence. The invention
CC      relates to the use of IL-20 for treating cervical cancer or cells
CC      infected with human papilloma virus. IL-20 can be administered alone or
CC      in conjunction with radiation or chemotherapeutic agents or surgical
CC      excision of the involved cells or lesions
XX
SQ      Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

US-10-789-251-26 (1-144) x ACF05161 (1-926)

Qy         1 CysValIleAlaThrAsnLeuGlnGlnIleArgAsnGlyPheSerAspIleArgGlySer 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 TGTGTGATCGCCACAAACCTTCAGCAAATACGAAATGGATTTTCTGACATACGGGCAGT 200

Qy        21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260

Qy        41 AspThrLysProIleAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       261 GACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGAC 320

Qy        61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       321 AGGGTATTTAAAAACTACCAGACACCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy        81 AlaAsnSerPheLeuThrIleLeuLysAspArgLeuCysHisLysAlaHisMetThrCys 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       381 GCCAATTCCTTTCTTACCATCAAGAAGAGGCTCCGCGCTCTGTCATGCCCACACATGACATGC 440

Qy       101 HisCysGlyGlyGlyGluAlaMetLysAspLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       441 CATTGTGGCGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

Qy       121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       501 GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG 560

Qy       141 GluGluThrGlu 144
             ||||||||||||
```

```
Db          561 GAGGAGACAGAA 572

RESULT 5
AAD61821
ID      AAD61821 standard; cDNA; 926 BP.
XX
AC      AAD61821;
XX
DT      15-JAN-2004 (first entry)
XX
DE      Human cytokine-like polypeptide-10 (Zcyto10) cDNA.
XX
KW      Human; cytokine-like polypeptide-10; Zcyto10; therapy; thrombocytopaenia;
KW      autoimmune disease; insulin-dependent diabetes mellitus; immune response;
KW      rheumatoid arthritis; multiple sclerosis; infection; radiation therapy;
KW      asthma; bronchitis; wound healing; Periodontal disease; antiinflammatory;
KW      psoriasis; eczema; dry skin; oral cavity; muscle atrophy; haemostatic;
KW      cancer; vulnerary; chromosome 1; gene; ss.
XX
OS      Homo sapiens.
XX
FH      Key             Location/Qualifiers
FT      CDS             45..575
FT                      /*tag= a
FT                      /product= "Human Zcyto10"
FT      sig_peptide     45..116
FT                      /*tag= b
FT      mat_peptide     117..572
FT                      /*tag= c
FT                      /product= "Mature human Zcyto10"
XX
PN      US6576743-B1.
XX
PI      Conklin DC, Haldeman BA;
XX
PA      (ZYMO ) ZYMOGENETICS INC.
XX
PT      Disclosure; Col 29-30; 0pp; English.
XX
PD      10-JUN-2003.
XX
DR      WPI; 2003-799828/75.
DR      P-PSDB; ABW00889.
XX
PF      17-MAY-1999; 99US-00313458.
XX
PR      26-NOV-1997; 97US-0066597P.
PR      25-NOV-1998; 98US-00199586.
XX
PT      Novel human cytokine-like polypeptide-10, Zcyto10, useful for treating
PT      insulin-dependent diabetes mellitus, rheumatoid arthritis, multiple
PT      sclerosis, asthma, psoriasis and inhibiting cancer cell growth.
XX
CC      The invention relates to an isolated human cytokine-like polypeptide-10
CC      (Zcyto10) polypeptide. Zcyto10 is useful for prevention or treatment of
CC      conditions characterised by improper cell proliferation, cell
CC      differentiation or cytokine production. Zcyto10 is useful for treating
CC      autoimmune diseases such as insulin-dependent diabetes mellitus,
CC      rheumatoid arthritis, multiple sclerosis, etc.; by inhibiting cellular
CC      immune response. The invention is useful for inhibiting cancer cell
CC      growth or proliferation, for stimulating immune system to combat
CC      microbial or viral infections, for increasing platelet production, and
CC      thus useful in cancer patients who experience thrombocytopaenia due to
CC      cancer therapy or radiation therapy. Zcyto10 is useful in trachea-
CC      specific or tracheobronchial-specific applications, such as in the
CC      maintenance or would repair of the tracheobronchial epithelium or cells
CC      underlying the same, in regulating mucous production or mucociliary
CC      clearance of debris or in treatment of asthma, bronchitis or other
CC      diseases of the tracheobronchial tract. Zcyto10 may also enhance wound
CC      healing and promote regeneration of affected tissues which may be
CC      especially useful in the treatment of periodontal disease. Zcyto10 can be
CC      used to treat skin conditions such as psoriasis, eczema and dry skin in
CC      general. Zcyto10 is useful for regenerating gastrointestinal tract or
```

```
CC    oral cavity and for modulating muscle tone in the tracheobronchial tract,
CC    and for treating muscle atrophy in the elderly, sick or bed-ridden.
CC    Zcyto10 is also useful for promoting wound healing. The present sequence
CC    is human Zcyto10 cDNA. The Zcyto10 gene is located on chromosome 10.
XX
SQ    Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score:              1.17e-86       Length:          926
Percent Similarity: 753.00         Matches:         144
Best Local Similarity: 100.00%     Conservative:    0
Query Match:        100.00%        Mismatches:      0
DB:                 100.00$        Indels:          0
                    10             Gaps:            0

US-10-789-251-26 (1-144) x AAD61821 (1-926)

Qy      1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GACACAAAGCCTCCGAATCGATCGCTGCCTCCGGCCCATTGCTAAGACTCTTATCTGGAC 20

Qy     21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGGCAGT 200

Qy     41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuLeuArgLeuTyrLeuAsp 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260

Qy     61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgGlyIleSerSerLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 GACACAAAGCCTCCGAATCGATCGCTGCCTCCGGCCCATTGCTAAGACTCTTATCTGGAC 320

Qy     81 AlaAsnSerPheLeuThrIleLeuLysAspLeuArgLeuCysHisSerAlaHisMetThrCys 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 AGGGTGATTTTAAAAACTACCAGACCCCTGACCATTATAACTCTCCGGAAGATCAGCAGCCTC 380

Qy    101 HisCysGlyGluGlnIleLeuMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381 GCCAATTCCTTTCTTACCATCAAGAAGGAACCTCCGGCTCTGTCATGCCCACATGACATGC 440

Qy    121 GluProGlnAlaAlaLeuAlaValLysGluAlaLeuGlyLeuAsnIleLeuLeuLeuGlnTrpMet 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    441 CATTGTGGGGAGGAAGCAATGAAGAAATAACAGCCAGAATTCTGAGTCCACTTTGAAAAGCTG 500

Qy    141 GluGluThrGlu 144
          ||||||||||||
Db    501 GAACCTCAGGCACGCAGTTGTGAAGGCTTTGGGGGGAACTAGACAATTCTTCTGCAATGGATG 560

Db    561 GAGGAGACAGAA 572
```

```
FT   mat_peptide        117..572
FT                      /*tag= c
FT                      /product= "Human mature Zcyto10 protein"
XX
FT                      US2003176557-A1.

PN   18-SEP-2003.
XX
PD   15-APR-2003; 2003US-00413661.
XX
PI   Conklin DC,  Haldeman BA;
XX
PA   (CONK/) CONKLIN D C,
PA   (HALD/) HALDEMAN B A.
XX
PR   26-NOV-1997;   97US-0065597P.
PR   25-NOV-1998;   98US-00199586.
PR   17-MAY-1999;   99US-00313458.
XX
PT   Novel isolated mammalian cytokine-like polypeptide-10 (Zcyto10), useful
PT   for treating asthma, bronchitis and other tracheobronchial damage.
XX
DR   WPI; 2003-863865/80.
DR   P-PSDB; ADG46669, ADG46679.
XX
PS   Disclosure; SEQ ID NO 1; 31pp; English.
XX
CC   The present invention relates to novel mammalian cytokine-like
CC   polypeptide-10 (Zcyto10) proteins and polynucleotides encoding such
CC   proteins. Sequences of the invention are useful for promoting the healing
CC   of wounds and for stimulating the proliferation of platelets. In
CC   particular Zcyto10 polypeptides may be used in trachea-specific or
CC   tracheobronchial-specific applications such as maintenance or wound
CC   repair of the tracheobronchial epithelium or cells underlying it; in
CC   regulating mucous production; mucociliary clearance of debris; in
CC   treatment of asthma, bronchitis and other diseases of the
CC   tracheobronchial tract. They are also used to promote regeneration of
CC   affected tissues which may be especially useful in the treatment of
CC   periodontal disease. Zcyto10 polypeptides can be used to treat skin
CC   conditions such as psoriasis, eczema and dry skin in general. They are
CC   also used in protein therapy. The present sequence is human Zcyto10 DNA.
XX
SQ   Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score:              1.17e-86       Length:          926
Percent Similarity: 753.00         Matches:         144
Best Local Similarity: 100.00%     Conservative:    0
Query Match:        100.00%        Mismatches:      0
DB:                 100.00$        Indels:          0
                    10             Gaps:            0

US-10-789-251-26 (1-144) x ADG46668 (1-926)

Qy      1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGGCAGT 200

Qy     21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260

Qy     41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuLeuArgLeuTyrLeuAsp 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 GACACAAAGCCTCCGAATCGATCGCTGCCTCCGGCCCATTGCTAAGACTCTTATCTGGAC 320

Qy     61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgGlyIleSerSerLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 AGGGTGATTTTAAAAACTACCAGACCCCTGACCATTATAACTCTCCGGAAGATCAGCAGCCTC 380

Qy     81 AlaAsnSerPheLeuThrIleLeuLysAspLeuArgLeuCysHisSerAlaHisMetThrCys 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381 GCCAATTCCTTTCTTACCATCAAGAAGGAACCTCCGGCTCTGTCATGCCCACATGACATGC 440
```

```
RESULT 6
ID   ADG46668 standard; DNA; 926 BP.
XX
AC   ADG46668;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human Zcyto10 DNA #1.
XX
KW   cytokine-like polypeptide-10; Zcyto10; wound healing;
KW   platelet proliferation; wound repair; mucous production; asthma;
KW   bronchitis; tracheobronchial tract disease; periodontal disease;
KW   skin condition; psoriasis; eczema; dry skin; protein therapy; human;
KW   vulnerary; respiratory; antibronchitic; dental; dermatological; gene; ds.
OS   Homo sapiens.

FH   Key            Location/Qualifiers
FT   CDS            45..575
FT                  /*tag= b
FT                  /product= "Human Zcyto10 protein"
XX
FT   sig_peptide    45..116
FT                  /*tag= a
```

Qy   101   HisCysGlyGlyGluGluAlaMetLeuLysTyrSerGlnIleLeuSerHisPheGluLysLeu   120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   441   CATTGTGGCGGAGGAGAAGCAATGAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG   500

Qy   121   GluProGlnAlaAlaValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet   140
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501   GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG   560

Qy   141   GluGluThrGlu   144
        ||||||||||||
Db   561   GAGGAGACAGAA   572

RESULT 7
ADQ88066

ID   ADQ88066 standard; DNA; 926 BP.
XX
AC   ADQ88066;
XX
DT   07-OCT-2004 (first entry)
XX
DE   Human Zcyto10 longer form DNA.
XX
KW   Mammalian cytokine-like polypeptide-10; Zcyto10; cell proliferation;
KW   cell differentiation; cytokine production; autoimmune disease;
KW   insulin dependent diabetes mellitus; multiple sclerosis;
KW   rheumatoid arthritis; cancer; wound healing; tissue regeneration;
KW   platelet count; asthma; skin disease; psoriasis; eczema; dry skin;
KW   antidiabetic; neuroprotective; antirheumatic; antiarthritic; cytostatic;
KW   immunostimulant; vulnerary; antiasthmatic; antipsoriatic; dermatological;
KW   gene therapy; human; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   45..575
FT   /*tag= b
FT   /product= "Human Zcyto10 protein"
FT   sig_peptide   45..116
FT   /*tag= a
FT   mat_peptide   117..572
FT   /*tag= c
FT   /product= "Human mature Zcyto10 protein"
FT   CDS   141..575
FT   /*tag= d
FT   /product= "Human Zcyto10 protein fragment"
FT   /partial
FT   /note= "No start codon"
XX
PN   US2004142428-A1.
XX
PD   22-JUL-2004.
XX
PF   27-FEB-2004; 2004US-00789129.
XX
PR   26-NOV-1997; 97US-0066597P.
PR   25-NOV-1998; 98US-0199586.
PR   15-APR-2003; 2003US-00413661.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Conklin DC, Haldeman BA;
XX
DR   WPI; 2004-552564/53.
DR   P-PSDB; ADQ88067, ADQ88077, ADQ88091.
XX
PT   New Zcyto10 polypeptides and polynucleotides, useful for treating
PT   autoimmune diseases (e.g. insulin dependent diabetes mellitus, multiple
PT   sclerosis or rheumatoid arthritis), or skin conditions (e.g. psoriasis or
PT   eczema).
XX
PS   Disclosure; SEQ ID NO 1; 31pp; English.
XX

CC   The present invention provides mammalian cytokine-like polypeptide-10
CC   (Zcyto10) proteins and their encoding polynucleotides. The invention is
CC   useful for treating conditions characterised by improper cell
CC   proliferation, cell differentiation or cytokine production, specifically
CC   for treating autoimmune diseases such as insulin dependent diabetes
CC   mellitus, multiple sclerosis and rheumatoid arthritis and for inhibiting
CC   cancer cell growth. The invention is also used to stimulate the immune
CC   system, to enhance wound healing and promote regeneration of affected
CC   tissues, to increase platelet count and to treat asthma and skin
CC   conditions such as psoriasis, eczema and dry skin. The invention acts as
CC   an antidiabetic, neuroprotective, antirheumatic, antiarthritic,
CC   cytostatic, immunostimulant, vulnerary, antiasthmatic, antipsoriatic and
CC   dermatological agent. The invention is also used in gene therapy. The
CC   present sequence is human Zcyto10 longer form DNA.
XX
SQ   Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   1.17e-86   Length: 926
Score: 753.00   Matches: 144
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 12   Gaps: 0

US-10-789-251-26 (1-144) x ADQ88066 (1-926)

Qy   1   CysValIleAlaThrAsnLeuGlnIleLeuArgAsnGlyPheSerAspIleArgGlySer   20
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141   TGTGTGATCGCCACAAACCTTCAGGAAAATACAGAAATGGGATTTTCTGACAATACGGGCAGT   200

Qy   21   ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln   40
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201   GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA   260

Qy   41   AspThrLysProAlaAsnArgCysGlySerLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp   60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261   GACACAAAGCCTGCCAATCGATGCGGCTCCCTCCTGCGCCATTTGCTAAGACTTCTATCTGGAC   320

Qy   61   ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu   80
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321   AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCACCCTC   380

Qy   81   AlaAsnSerPheLeuThrIleLeuLysAspLeuArgLeuCysHisAlaHisMetThrCys   100
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381   GCCAATTCCTTTCTTACCATCAAGAAGACCTCCGGCTTCTGTCATGCCCACATGACATGC   440

Qy   101   HisCysGlyGlyGluGluAlaMetLeuLysTyrSerGlnIleLeuSerHisPheGluLysLeu   120
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441   CATTGTGGCGGAGGAGAAGCAATGAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG   500

Qy   121   GluProGlnAlaAlaValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet   140
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501   GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATG   560

Qy   141   GluGluThrGlu   144
       ||||||||||||
Db   561   GAGGAGACAGAA   572

RESULT 8
ADR16327

ID   ADR16327 standard; DNA; 926 BP.
XX
AC   ADR16327;
XX
DT   21-OCT-2004 (first entry)
XX
DE   Human cytokine-like polypeptide-10; Zcyto10 long form DNA.
XX
KW   Cytokine-like polypeptide-10; Zcyto10; therapy; asthma; infection;
KW   psoriasis; eczema; dry skin; wound healing; platelet proliferation;
KW   human; gene; ds.
XX

OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT
FT   CDS   45..575
FT   /product= b
XX
FT   sig_peptide   45..116
FT   /tag= a
FT   /product= "Zcyto10 long form protein"
FT
FT   mat_peptide   117..572
FT   /tag= c
FT   /product= "Mature Zcyto10 long form protein"
XX
PN   US20040152878-A1.
XX
PD   05-AUG-2004.
XX
PF   27-FEB-2004; 2004US-00789968.
XX
PR   26-NOV-1997; 97US-0066597P.
PR   25-NOV-1998; 98US-00199586.
PR   15-APR-2003; 2003US-00413661.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Conklin DC, Haldeman BA;
XX
DR   WPI; 2004-580197/56.
DR   P-PSDB; ADR16328, ADR16338.
XX
PT   New isolated antibody that binds to a Zcyto10 polypeptide, useful for
PT   treating asthma, microbial or viral infections, and for promoting the
PT   healing of wounds, psoriasis, eczema or dry skin.
XX
PS   Disclosure; SEQ ID NO 1; 32pp; English.
XX
CC   The invention relates to novel cytokine-like polypeptide-10 (Zcyto10)
CC   polypeptides and polynucleotides. Zcyto10 sequences are useful for
CC   treating asthma, microbial or viral infections, psoriasis, eczema or dry
CC   skin, for promoting the healing of wounds and for stimulating the
CC   proliferation of platelets. The present sequence is human Zcyto10 DNA.
XX
SQ   Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   1.17e-86   Length: 926
Score: 753.00   Matches: 144
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13   Indels: 0
DB: Gaps: 0

US-10-789-251-26 (1-144) x ADR16327 (1-926)

```
Qy      1 CysValIleAlaThrAsnLeuGlnIleLeuArgAsnGlyPheSerAspIleArgGlySer 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGCAGT 200

Qy     21 ValGlnIleAlaLysGlyAsnIleLeuArgIleLeuArgArgThrGluSerLeuGln 40
Db    201 GTGCAAGCCAAAGATGGAAACATTGACATCAGATCTTAAGGAGGACTGAGTCTTTGCAA 260

Qy     41 AspThrLysProAlaAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
Db    261 GACACAAAGCCTCGGAATCGATCGCTTCCTCCGCCATTGCTAAGACTCTTATCTGGAC 320

Qy     61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgGlyLysIleSerSerLeu 80
Db    321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC 380

Qy     81 AlaAsnSerPheLeuThrIleLysLysAspLeuAspLeuCysHisSerAlaHisMetThrCys 100
Db    381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTCGGTCTGTCATGCCACATGACATGC 440
```

Qy   101 HisCysGlyGluGluGluAlaMetLysLysTyrSerGlnIleLeuLeuSerHisPheGlyLysLeu 120
Db   441 CATTGTGGGGAGGAGGAGGCAAATGAAGAAATACAGCCAGATTCTAGTCACTTTGAAAAACCTG 500

Qy   121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
Db   501 GAACCTCAGGCAGCCAGCAGTTGTGAAAGCGCTTGGGGAGCTAGACATTCTTCTGCAAATGGATG 560

Qy   141 GluGluThrGlu 144
Db   561 GAGGAGACAGAA 572

RESULT 9
ADR24325
ID   ADR24325 standard; DNA; 926 BP.
XX
AC   ADR24325;
XX
DT   21-OCT-2004 (first entry)
XX
DE   Breast cancer prognosis marker #186.
XX
KW   d8; breast cancer; prognosis; gene expression; diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO200406545-A2.
XX
PD   05-AUG-2004.
XX
PF   15-JAN-2004; 2004WO-US001100.
XX
PR   15-JAN-2003; 2003US-00342887.
XX
PA   (ROSB-) ROSETTA INPHARMATICS LLC.
PA   (NECA-) NETHERLANDS CANCER INST.
XX
PI   Van't Veer LJ, He Y;
XX
DR   WPI; 2004-593473/57.
XX
PT   Classifying a breast cancer patient according to prognosis comprises
PT   determining the similarity between the level of expression of each of
PT   five genes in a cell sample taken from patient, to control levels.
XX
PS   Disclosure; SEQ ID NO 186; 226pp; English.
XX
CC   The invention relates to a method of classifying a breast cancer patient
CC   according to prognosis by determining the similarity between the level of
CC   expression of each of five genes for which markers are listed in the
CC   specification, in a cell sample taken from the breast cancer patient, to
CC   control levels of expression for each respective five genes to obtain a
CC   patient similarity value. The methods are useful for classifying a breast
CC   cancer patient according to prognosis. Kits and computer program products
CC   are useful for data analysis using the diagnostic, prognostic and
CC   statistical methods of the invention. This sequence corresponds to a
CC   marker used in the method of the invention.
XX
SQ   Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   1.17e-86   Length: 926
Score: 753.00   Matches: 144
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13   Indels: 0
DB: Gaps: 0

US-10-789-251-26 (1-144) x ADR24325 (1-926)

```
Qy      1 CysValIleAlaThrAsnLeuGlnIleLeuArgAsnGlyPheSerAspIleArgGlySer 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGCAGT 200
```

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 201 GTGCAAGCCAAAGATGGAAACAATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisIleLeuLeuLeuTyrLeuAsp 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 261 GACACAAAGCCTGCGAATCGATGCTGCCTCCTCCGGCATCCTTGCTAAGACTCTATCTGAC 320

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisThrTyrThrLeuArgLysIleSerSerLeu 80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTTCTCCGGAAGATCAGCAGCCTC 380

Qy   81 AlaAsnSerPheLeuThrIleLysLysTyrLysAspLeuArgLeuCysHisIleAlaHisMetThrCys 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 381 GCCAATTCCTTTCTTACCATCAAGAAGTACAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440

Qy 101 HisCysGlyGluGlnIleAlaMetLeuLysTyrSerGlnIleIleLeuSerHisPheGlyLysLeu 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 441 CATTGTGGGGAGCAAATAGCAATGCTCAAGTACAGCCAGATTATACTCCACTTTGAAAAGCTG 500

Qy 121 GluProGlnAlaLysAlaValValLysGlnLeuGlyLeuAspIleLeuLeuGlnTrpMet 140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 501 GAACCTCAGGCAGCAGTTGTGAAGCGTTTGGGGGGGAACTAGACAATTCTTCTGCAATGGATG 560

Qy 141 GluGluThrGlu 144
        ||||||||||||
Db 561 GAGGAGACAGA 572

RESULT 10

ID ADS18362 standard; DNA; 926 BP.
XX
AC ADS18362;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human Zcyto10 protein encoding DNA #1.
XX
KW Zcyto10; cytokine-like polypeptide; cell proliferation;
KW cell differentiation; autoimmune disease; multiple sclerosis;
KW rheumatoid arthritis; asthma; psoriasis; cancer; wound; gene therapy;
KW immunosuppressive; antidiabetic; neuroprotective; antirheumatic;
KW antiarthritic; antiasthmatic; antipsoriatic; cytostatic; vulnerary;
KW human; gene; chromosome 1q32.2; d8.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   45..575
FT   /tag= b
FT   /product= "Zcyto10 protein "
FT sig_peptide   45..116
FT   /tag= a
FT mat_peptide   117..572
FT   /tag= c
FT   /product= "Mature Zcyto10 protein"
XX
PN US2004181040-A1.
XX
PD 16-SEP-2004.
XX
PF 29-DEC-2003; 2003US-00748484.
XX
PR 26-NOV-1997; 97US-0066597P.
PR 25-NOV-1998; 98US-0199586.
PR 15-APR-2003; 2003US-00413661.
XX
PA (CONK/) CONKLIN D C.
PA (HALD/) HALDEMAN B A.
PA (GROS/) GROSSMANN A.
XX
PI Conklin DC, Haldeman BA, Grossmann A;

XX
DR WPI; 2004-667683/65.
DR P-PSDB; ADS18363, ADS18373.
XX
PT New antibody that selectively binds to a Zcyto10 polypeptide useful for
PT modulating cell proliferation, cell differentiation or cytokine
PT production in the prevention or treatment of e.g. autoimmune diseases,
PT cancer or wounds.
XX
PS Disclosure; SEQ ID NO 1; 31pp; English.

CC The present invention relates to a mammalian cytokine-like polypeptide,
CC Zcyto10 and its encoding polynucleotide. The invention is useful for
CC modulating cell proliferation, cell differentiation or cytokine
CC production in the prevention or treatment of conditions such as
CC autoimmune diseases (e.g. diabetes, multiple sclerosis, rheumatoid
CC arthritis, asthma or psoriasis) and cancer or wounds. The invention is
CC also useful in gene therapy. The present sequence is the human Zcyto10
CC protein encoding DNA. This Zcyto10 gene is located on chromosome 1q32.2.
XX
SQ Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

US-10-789-251-26 (1-141) x ADS18362 (1-926)

Alignment Scores:
Pred. No.:   1.17e-86   Length: 926
Score: 753.00   Matches: 144
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 13   Indels: 0
DB: Gaps: 0

Qy   1 CysValIleAlaThrAsnLeuGlnHisIleArgAsnGlyPheSerAspIleArgGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 141 TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGGTCT 200

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 201 GTGCAAGCCAAAGATGGAAACAATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisIleLeuLeuLeuTyrLeuAsp 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 261 GACACAAAGCCTGCGAATCGATGCTGCCTCCTCCGGCATCCTTGCTAAGACTCTATCTGAC 320

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisThrTyrThrLeuArgLysIleSerSerLeu 80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTTCTCCGGAAGATCAGCAGCCTC 380

Qy   81 AlaAsnSerPheLeuThrIleLysLysTyrLysAspLeuArgLeuCysHisIleAlaHisMetThrCys 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 381 GCCAATTCCTTTCTTACCATCAAGAAGTACAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440

Qy 101 HisCysGlyGluGlnIleAlaMetLeuLysTyrSerGlnIleIleLeuSerHisPheGlyLysLeu 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 441 CATTGTGGGGAGCAAATAGCAATGCTCAAGTACAGCCAGATTATACTCCACTTTGAAAAGCTG 500

Qy 121 GluProGlnAlaLysAlaValValLysGlnLeuGlyLeuAspIleLeuLeuGlnTrpMet 140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 501 GAACCTCAGGCAGCAGTTGTGAAGCGTTTGGGGGGGAACTAGACAATTCTTCTGCAATGGATG 560

Qy 141 GluGluThrGlu 144
        ||||||||||||
Db 561 GAGGAGACAGA 572

RESULT 11

AEA50048
ID AEA50048 standard; cDNA; 926 BP.
XX
AC AEA50048;
XX
DT 11-AUG-2005 (first entry)
XX
DE Full length IL-20 coding sequence.

```
XX
KW   ss; gene; Antiinflammatory; Gastrointestinal-Gen.; Antiulcer;
KW   Antiarthritic; Dermatological; Antipsoriatic; Antibacterial;
KW   Immunosuppressive; Antimicrobial; IL-Antagonist-20; Interleukin-20;
KW   IL-20; inflammation; inflammatory bowel disease; ulcerative colitis;
KW   Crohns disease; arthritis; atopic dermatitis ; psoriasis; endotoxemia;
KW   septicemia; toxic shock syndrome ; infectious disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             45..575
FT                   /tag= a
XX
DR   WO200505200-A2.
XX
PN   09-JUN-2005.
XX
PF   19-NOV-2004; 2004WO-US039071.
XX
PR   21-NOV-2003; 2003US-0524131P.
PR   24-MAR-2004; 2004US-0555857P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Xu W, Kindsvogel WR,  Chen Z,  Hughes SD, Chandrasekher YA;
PI   Dillon SR, Lehner JM, Siadak AW, Sivakumar PV, Moore MD;
XX
DR   WPI; 2005-405359/41.
DR   P-PSDB; AEA50049, AEA50050.
XX
PT   Example 1; SEQ ID NO 1; 268pp; English.
XX
PT   This sequence encodes full length interleukin-20 (IL-20), longer form IL-
PT   20x1. The method of the invention for producing an antibody to IL-20
PT   comprises inoculating an animal with an IL-20 polypeptide which elicits
PT   an immune response in the animal to produce the antibody, and isolating
PT   the antibody from the animal. The antibody is useful for treating a
PT   pathological condition in a subject associated with IL-20 activity such
PT   as chronic inflammatory condition, specifically inflammatory bowel
PT   disease, ulcerative colitis, Crohns disease, arthritis, atopic
PT   dermatitis and psoriasis, or acute inflammatory condition such as
PT   endotoxemia, septicemia, toxic shock syndrome and infectious disease. An
PT   antagonist of IL-20 is useful for treating a mammal afflicted with an
PT   inflammatory disease in which IL-20 plays a role such that the
PT   inflammation is reduced, where the antagonist comprises an antibody,
PT   antibody fragment, or binding polypeptide that specifically binds a
PT   polypeptide or polypeptide fragment of IL-20 or a polypeptide or
PT   polypeptide fragment of IL-20, and where the inflammatory activity of IL-
PT   20 is reduced. The method is useful for producing such therapeutic
PT   antibody. The antibody or antibody fragment, produced using the above
PT   method, binds to IL-20, and inhibits or reduces the pro-inflammatory
PT   activity of IL-20. IL-20-induced proliferation or differentiation of
PT   hematopoietic cells and hematopoietic cell progenitors may be reduced or
PT   inhibited using the antibody.
XX
SQ   Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
```

Alignment Scores:

Pred. No.:

Score:	1.17e-86
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	14
DB:	

Length:	926
Matches:	144
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-789-251-26 (1-144) x AEA50048 (1-926)

```
Qy    1 CysValIleAlaThrAsnLeuGlnLeuLeuArgAsnGlyPheSerAspIleArgGlySer  20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141 TGTGTGATCGCCACAAACCTTCAGGAAAATACGAAATGGGATTTTCTGACTAACTACGCAGT 200

Qy   21 ValGlnAlaLysAspGlyAsnIleLeuAspIleLeuArgIleLeuArgArgThrGluSerLeu 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201 GTGCAAGCCAAAGATGGAAACATTGAACATTGACATCAGAATCCTTAGGAGGACTGAGTCTTTGCAA 260

Qy   41 AspThrLysProAlaAsnArgCysTyrCysLeuLeuLeuArgHisLeuLeuTyrLeuAsp   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261 GACACAAAGCCTGCGAATCGATGCTACTGCCTCCTGCTGCGCCATTTGCTAAGCTTTATCTGGAC 320

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu   80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  321 AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTC   380

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys  100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  381 GCCAATTCCTTTCTTACCATCAAGAAGGACCTTCGGCTCTGCCACGCCCATATGACATGC  440

Qy  101 HisCysGlyGlyAsnLeuAlaMetLysTyrSerGlnIleLeuSerHisPheGluLysLeu  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  441 CATTGTTGGGGAGGAAACCTAGCAATGAAGTACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

Qy  121 GluProGlnAlaAlaValValLysSerAlaLeuLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  501 GAACCTCAGGCAGCAGTTGTGAAGTCTGCTCTTTGGGGGAGACTAGACATTCTTCTGCAATGGATG 560

Qy  141 GluGluThrGlu 144
          ||||||||||||
Db  561 GAGGAGACAGAA 572
```

```
RESULT 12
AEA28786
ID   AEA28786 standard; cDNA; 926 BP.
XX
AC   AEA28786;
XX
DT   11-AUG-2005 (first entry)
XX
DE   Human interleukin 20 (IL-20) precursor cDNA clone.
XX
KW   antibody production; cytokine; antiinflammatory; gastrointestinal-gen.;
KW   antiulcer; antiarthritic; dermatological; antipsoriatic; antibacterial;
KW   immunosuppressive; antimicrobial; inflammation;
KW   inflammatory bowel disease; ulcerative colitis; Crohns disease;
KW   arthritis; atopic dermatitis; psoriasis; cancer; endotoxemia; sepsis;
KW   endotoxic shock; infectious disease; IL-20; interleukin-20; ss; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             45..575
FT                   /tag= a
FT                   /product= "Human interleukin 20 (IL-20) protein"
XX
PN   WO200505200-A2.
XX
PD   09-JUN-2005.
XX
PF   19-NOV-2004; 2004WO-US039097.
XX
PR   21-NOV-2003; 2003US-0524131P.
PR   24-MAR-2004; 2004US-0555857P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Xu W, Kindsvogel WR,  Chen Z,  Hughes SD, Chandrasekher YA;
PI   Dillon SR, Lehner JM, Siadak AW, Sivakumar PV, Moore MD;
XX
DR   WPI; 2005-405360/41.
DR   P-PSDB; AEA28787.
XX
```

PT   Producing an antibody to an interleukin 20RA (IL-20RA) polypeptide,
PT   useful for treating inflammatory diseases e.g. arthritis, by inoculating
PT   an animal with the polypeptide which elicits an immune response to
PT   produce the antibody.
XX
PS   Example 1; SEQ ID NO 1; 265pp; English.
XX
CC   The invention relates to a novel method for producing an antibody to a
CC   polypeptide. The method comprises inoculating an animal with a
CC   polypeptide selected from any of SEQ ID NO: 14, 15, 17 or 19 as given in
CC   the specification, where the polypeptide elicits an immune response in
CC   the animal to produce the antibody, and isolating the antibody from the
CC   animal. The antibody specifically binds to the pro-inflammatory cytokine
CC   interleukin 20 (IL-20 or Zcyto10), or one its receptors IL-20RA (ZcytpR7)
CC   or IL-20RB (pDIRS1). The method of the invention demonstrates
CC   antiinflammatory, gastrointestinal-gen., anticer, antiarthritic,
CC   antiinflammatory,
CC   dermatological, antipsoriatic, antibacterial, immunosuppressive and
CC   antimicrobial applications. The antibody may be useful for treating a
CC   pathological condition in a subject associated with IL-20RA, such as a
CC   chronic inflammatory condition selected from inflammatory bowel disease,
CC   ulcerative colitis, Crohn's disease, arthritis, atopic dermatitis and
CC   psoriasis, cancer, or an acute inflammatory condition such as
CC   endotoxemia, septicemia, toxic shock syndrome and infectious disease. The
CC   current sequence is that of a human IL-20 precursor cDNA clone of the
CC   invention.
XX
SQ   Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.17e-86		
Score:	753.00		
Percent Similarity:	100.00%	Matches:	926
Best Local Similarity:	100.00%	Conservative:	0
Query Match:	14	Mismatches:	0
DB:		Indels:	0
		Gaps:	0

US-10-789-251-26 (1-144) x AEA28786 (1-926)

```
Qy   1   CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141  TGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGACATACGGGGCAGT 200

Qy  21   ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201  GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAA 260

Qy  41   AspThrLysProAlaAsnArgCysHisLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261  GACACAAAGCCTGCGAATCGATGCTGCCTTCGCGCCATTTGCTAAGACTCTATCTGGAC 320

Qy  61   ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  321  AGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGAATCAGCAGCCTC 380

Qy  81   AlaAsnSerPheLeuThrIleLysTyrLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  381  GCCAATTCTTTCTTTACCATCAAGTACAAGGACCTCCGGCTCTGTCATGCCCACATGACATGC 440

Qy  101  HisCysGlyLysGlyHisTyrSerGlnIleLeuSerHisSPheGluLysLeuLeu 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  441  CATTGTGGGGAGGGAAGCAATGAAGAAATACAGCCAGAATTCTGAGTCACTTTGAAAAGCTG 500

Qy  121  GluProGlnAlaAlaValValLysAlaLeuGlyLysGluLeuGlnTrpMet 140
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  501  GAACCTCAGGCAGCAGTGTGGGGGAACTAGACAATTCTTCTGCAATGGATG 560

Qy  141  GluGluThrGlu 144
         ||||||||||||
Db  561  GAGGAGACAGAA 572
```

XX
AC   ABV75151;
XX
DT   19-FEB-2003 (first entry)
XX
DE   Human interleukin-20 (IL-20) codon optimised fragment zcyto10X1.
XX
KW   Protein synthesis; data mining; recombinant; interleukin-20; IL-20;
KW   human; ds.
XX
OS   Homo sapiens.
XX
PN   WO200283853-A2.
XX
PD   24-OCT-2002.
XX
PF   12-APR-2002; 2002WO-US011513.
XX
PR   13-APR-2001; 2001US-0283688P.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Powder TA, Chan C;
XX
DR   WPI; 2003-067576/06.
XX
PT   New polynucleotide, useful for producing a nucleic acid construct for
PT   expression of an amino acid sequence of interest.
XX
PS   Example 1; Page 36; 40pp; English.
XX
CC   The invention provides a new purified polynucleotide that comprises the
CC   nucleic acid sequence A-B-C-D-E; where: A= start codon, B= polynucleotide
CC   sequence of 13 nucleic acids, where the sequence has homology with 13
CC   base pair (bp) sequence, where at least 5 nucleic acids are identical to
CC   a 13 bp sequence (ABV75139), and where the nucleic acid sequence does not
CC   code for a stop codon, C= polynucleotide sequence comprising 10, 13, 16
CC   or 19 nucleic acids of a 19 bp sequence (ABV75140), D= polynucleotide
CC   sequence comprising 8 bp sequence (ABV75141), E= polynucleotide
CC   from 9 sequences (ABV75144-150) where at least 50% nucleotides are either
CC   adenine or thymine, and where only E encodes a stop codon. The
CC   polynucleotide is useful for producing a nucleic acid construct for
CC   expression of an amino acid sequence of interest. The present sequence
CC   represents a human interleukin-20 (IL-20) codon optimised fragment for
CC   expression in E. coli.
XX
SQ   Sequence 462 BP; 121 A; 131 C; 117 G; 93 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.38e-86		
Score:	749.00		
Percent Similarity:	100.00%	Matches:	462
Best Local Similarity:	99.31%	Conservative:	1
Query Match:	8	Mismatches:	0
DB:		Indels:	0
		Gaps:	0

US-10-789-251-26 (1-144) x ABV75151 (1-462)

```
Qy   1   CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
         |||||||||||||||||||||||||| :::|||||||||||||:||||||||||||||||
Db  28   TGTGTGATCGCCACAAACCTGCAGGAAATCCGTAACGGGTTTTCTGAGATCCGTGGCAGC 87

Qy  21   ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  88   GTGCAGGCCAAAGATGGTAACATTGACATCCGTATCCTGCGTCGTACCGAGTCTCTGCAG 147

Qy  41   AspThrLysProAlaAsnArgCysHisLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  148  GACACCAAACCGGCAAACCGTTGCTGCCTGCTGCGTCACCTGCTGCGTCTGTATCTGGAC 207

Qy  61   ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  208  CGTGTGTTTAAAAACTACCAGACCCCGGACCACTATACCCTGCGTAAAATCAGCAGCCTG 267
```

RESULT 14
AEB26649

ID   AEB26649 standard; DNA; 462 BP.
XX
AC   AEB26649;
XX
DT   08-SEP-2005 (first entry)
XX
DE   Human interleukin (IL)-20 DNA, SEQ ID NO: 18.
XX
KW   Expression; gene regulation; toxin; interleukin; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..462
FT   /*tag= a
FT   /product= "Human interleukin (IL)-20"
XX
PN   WO2005058946-A2.
XX
PD   30-JUN-2005.
XX
PR   12-DEC-2003; 2003US-0529412P.
XX
PF   10-DEC-2004; 2004WO-US041776.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Chan C, Powder TA;
XX
DR   WPI; 2005-479318/48.
DR   P-PSDB; AEB26650.
XX
PT   New Syn 1 and Syn 2 tight regulated synthetic promoters, useful for
PT   controlling uninduced, leaky expression of proteins that are toxic and
PT   interfere with production of recombinant protein from an Escherichia coli
PT   expression system.
XX
PS   Example 5; SEQ ID NO 18; 39pp; English.
XX
CC   The invention relates to Syn 1 and Syn 2 tight regulated synthetic
CC   promoters and methods for enhancing the expression of recombinant
CC   proteins. The Syn 1 and Syn 2 tight regulated synthetic promoters are
CC   useful for controlling uninduced, leaky expression of proteins that are
CC   toxic and interfere with production of recombinant protein from an
CC   Escherichia coli expression system. They are useful for controlling basal
CC   expression of target genes. The present sequence is the human interleukin
CC   (IL)-20 DNA. This sequence is used in the comparison of promoter
CC   strength.
XX
SQ   Sequence 462 BP; 121 A; 131 C; 117 G; 93 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   1.38e-86   Length: 462
Score: 749.00   Matches: 143

Qy   81 AlaAsnSerPheLeuThrIleLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
Db   268 GCCAACTCCTTCCTGACCATCAAAAAAGACCTGCGTCTGTGTCACGCCCACATGACCTGC 327

Qy   101 HisCysGlyGlyGluGlnIleLeuGluLeuSerHisPheGluLysLeu 120
Db   328 CACTGTGGTGGTGAGGAAGCAATGAAAAAATACAGCCAGATTCTGAGCCACTTCGAAAAACTG 387

Qy   121 GluProGlnAlaAlaValValLeuAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
Db   388 GAACCGCAGGCAGCAGTGGTTGAAGGTCTGGGTGAACTGGACATTCTGCTGCAGTGGATG 447

Qy   141 GluGluThrGlu 144
Db   448 GAGGAGACCGAA 459

Percent Similarity: 100.00%   Conservative: 1
Best Local Similarity: 99.31%   Mismatches: 0
Query Match: 99.47%   Indels: 0
DB: 14   Gaps: 0

US-10-789-251-26 (1-144) x AEB26649 (1-462)

Qy   1 CysValIleAlaThrAsnLeuGlnIleLeuArgAsnGlyPheSerAspIleArgGlySer 20
Db   28 TGTGTGATCGCGACCAACCTGCAGATAGAAATCCGTAACGGTTTCTCAGATATCCGTGGCAGC 87

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
Db   88 GTGCAGGCCAAAGATGGTAACATTGACATCCGTATCCTGCGTCGTACCGAGTCTCTGCAG 147

Qy   41 AspThrLysLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
Db   148 GACACCAAACCGGCAAACCGTTGCTGCCTGCTGCGGCCACCTGCTTCTGTATCTGGAC 207

Qy   61 ArgValPheLysAlaAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
Db   208 CGTGTTTTCAAAGCAAACTACCAGACCCCGGACCACTATACCCTGCGTAAAATCAGCAGCCTG 267

Qy   81 AlaAsnSerPheLeuThrIleLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
Db   268 GCCAACTCCTTCCTGACCATCAAAAAAGACCTGCGTCTGTGTCACGCCCACATGACCTGC 327

Qy   101 HisCysGlyGlyGluGlnIleLeuGluLeuSerHisPheGluLysLeu 120
Db   328 CACTGTGGTGGTGAGGAAGCAATGAAAAAATACAGCCAGATTCTGAGCCACTTCGAAAAACTG 387

Qy   121 GluProGlnAlaAlaValValLeuAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
Db   388 GAACCGCAGGCAGCAGTGGTTGAAGGTCTGGGTGAACTGGACATTCTGCTGCAGTGGATG 447

Qy   141 GluGluThrGlu 144
Db   448 GAGGAGACCGAA 459

RESULT 15
ABV75154

ID   ABV75154 standard; DNA; 513 BP.
XX
AC   ABV75154;
XX
DT   19-FEB-2003 (first entry)
XX
DE   EC sequence upstream of IL-20 codon optimised fragment zcyto10X1.
XX
KW   Protein synthesis; data mining; recombinant; interleukin-20; IL-20;
KW   human; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200283853-A2.
XX
PD   24-OCT-2002.
XX
PR   12-APR-2002; 2002WO-US011513.
XX
PF   13-APR-2001; 2001US-0283688P.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Powder TA, Chan C;
XX
DR   WPI; 2003-067576/06.
XX
PT   New polynucleotide, useful for producing a nucleic acid construct for
PT   expression of an amino acid sequence of interest.
XX
PS   Example 1; Page 37; 40pp; English.

XX
CC   The invention provides a new purified polynucleotide that comprises the
CC   nucleic acid sequence A-B-C-D-E; where: A= start codon, B= polynucleotide
CC   sequence of 13 nucleic acids, where the sequence has homology with 13
CC   base pair (bp) sequence, where at least 5 nucleic acids are identical to
CC   a 13 bp sequence (ABV75139), and where the nucleic acid sequence does not
CC   code for a stop codon, C= polynucleotide sequence comprising 10, 13, 16
CC   or 19 nucleic acids of a 19 bp sequence (ABV75140), D= polynucleotide
CC   sequence comprising 8 bp (ABV75141), E= polynucleotide sequence selected
CC   from 9 sequences (ABV75144-150) where at least 50% nucleotides are either
CC   adenine or thymine, and where only E encodes a stop codon. The
CC   polynucleotide is useful for producing a nucleic acid construct for
CC   expression of an amino acid sequence of interest. The present sequence
CC   represents a sequence comprising an expression cassette (EC)
CC   polynucleotide sequence inserted upstream of a human interleukin-20 (IL-
CC   20) codon optimised sequence fragment for expression in E. coli
XX
SQ   Sequence 513 BP; 143 A; 145 C; 126 G; 99 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score: 1.61e-86
Percent Similarity: 749.00   Length: 513
Best Local Similarity: 100.00%   Matches: 143
Query Match: 99.31%   Conservative: 1
DB: 99.47%   Mismatches: 1
                        8   Indels: 0
                                        Gaps: 0

US-10-789-251-26 (1-144) x ABV75154 (1-513)

Qy   1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer   20
          |||||||||||||||||||||||||||||||||||||||||||||||||||::|||||||
Db   79 TGTGTGATCGCCACCAACCTGCAGGAAATCCGTAACGGTTTCTCTGAGATCCGTGGCAGC 138

Qy   21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgAsnThrGluSerLeuGln   40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   139 GTGCAGGCCAAAGATGGTAACATTGACATCCGTATCCTGCGTAACACCGAGTCTCTGCAG 198

Qy   41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   199 GACACCAAACCGGCGAACCGTTGCTGCCTGCTGCGCCACCTGCTGCGTCTGTATCTGGAC 258

Qy   61 ArgValPheLysAsnTyrGlnThrProAspHisThrTyrThrLeuArgLysIleSerLeu   80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   259 CGTGTTTTCAAAAACTACCAGACACCCGACCATACCTACACTCTGCGTAAAATCAGCCTG 318

Qy   81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   319 GCCAACTCCTTCCTGACCATCAAAAAAGACCTGCGTCTGTGTCACGCCCACATGACCTGC 378

Qy   101 HisCysGlyGlyUlaMetLysGlyTyrSerGlnIleLeuSerHisPheGluLysLeu   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   379 CACTGTGGTGAGGAGCAATGAAAAAAATACAGCCAGATTCTGAGCCACTTCGAAAAACTG 438

Qy   121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet 140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   439 GAACCGCAGGCAGCAGTGGTGAAAGCTCTGGGTGAACTGGACATTCTGCTGCAGTGGATG 498

Qy   141 GluGluThrGlu 144
          ||||||||||
Db   499 GAGGAGACCGAA 510

Search completed: December 28, 2005, 11:56:33
Job time : 505 secs